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AC AAB12236;
 XX
 DT 10-NOV-2000 (first entry)
 XX
 DE Partial sequence of HIV-1 strain ESS gp41 immunodominant region.
 XX
 KM HIV-1; AIDS; human immunodeficiency virus type 1; immunodominant region;
 XX acquired immunodeficiency syndrome; group O HIV; gp41; ESS.
 OS Human immunodeficiency virus type 1.
 XX
 PN EP1013766-A2.
 PD 28-JUN-2000.
 XX
 PF 29-NOV-1999; 99EP-0309491.
 XX
 PR 30-NOV-1998; 98US-0110292.
 PR 08-FEB-1999; 99US-0119138.
 PR 04-NOV-1999; 99US-0433428.
 XX
 PA (ORTH-) ORTHO-CLINICAL DIAGNOSTICS INC.
 XX
 PI De Lays R, Zheng J;
 XX
 DR WPI; 2000-402205/35.
 XX
 PT New antigenic peptides and peptide functional derivatives, useful for
 PT detection of antibodies produced in response to human immunodeficiency
 PT virus group O antibodies -
 XX
 PS Example 1; Fig 1; 52pp; English.
 PS
 CC The present sequence is a partial gp41 protein of human immunodeficiency
 CC virus type 1 (HIV-1) strain ESS. HIV is the principle aetiological
 CC agent for acquired immunodeficiency syndrome (AIDS). gp41 is a HIV
 CC envelope protein, and may be used as an antigen for the detection of
 CC antibodies produced in response to HIV infection. ESS is a member of
 CC HIV group O (outlier). The present sequence is the immunodominant region
 CC of gp41. This sequence was used in a sequence homology alignment,
 CC which in turn was used to derive a consensus sequence peptide: peptide
 CC 147 (AAB12235).
 CC
 XX
 SQ Sequence 33 AA:
 SQ
 Query Match 75.7%; Score 131; DB 21; Length 33;
 Best Local Similarity 75.0%; Pred. No. 8.2e-12;
 Matches 21; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
 QY 3 ETLMDODORLNSGCKGRITCYTSARWH 30
 DB 6 etllqngqllnswgckgrivcytsvkn 33
 XX
 RESULT 12
 AAM07343
 ID AAM07343 standard; peptide: 40 AA.
 XX
 AC AAM07343;
 XX
 DT 03-JUN-1997 (first entry)
 XX
 DE Partial sequence of gp41 from HIV-1 gp. O strain BCF02 (ESS).
 XX
 KM Human immunodeficiency virus type 1; HIV-1; envelope; group M; group O;
 KM C2V3-env; gp41; gag; retrovirus; strain; gp120; hypervariable loop;
 KM primer; hybridisation; amplification; PCR; polymerase chain reaction;
 KM immunogen; antibody.
 XX
 OS Human immunodeficiency virus type 1.
 XX
 PN W09627013-

XX
 PD 06-SEP-1996.
 XX
 PF 26-FEB-1996; 96WO-FR00294.
 XX
 PR 27-FEB-1995; 95FR-0002236.
 XX
 PA (ASSI-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.
 PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 XX
 PI Chaux-Baudier ML, Lousset-Ajaka I, Ly T, Saragosti S, Simon F;
 XX
 DR WPI; 1996-412779/41.
 DR N-PSDB; AAT44918.
 XX
 PT New strains of HIV-1 group O, related DNA fragments, peptide(s) and
 PT antibodies - useful for diagnosis, screening and typing, or as
 PT immunogens
 XX
 PS Claim 12; Page 33; 71pp; French.
 PS
 CC Human immunodeficiency virus type 1 (HIV-1) strains are currently
 CC divided into 2 major groups based on the nucleotide sequences of the
 CC envelope gene (env): group M containing sub-groups A-G, and group O
 CC containing the strains AM70 and WPS180. The invention relates to the
 CC discovery of several new strains of HIV-1 which can be placed in group O,
 CC based on the partial sequences of the C2V3-env, gp41 and gag genes (see
 CC AM744907-39 and AAM07329-64). The novel strains have been deposited as
 CC retroviruses CCMC I-1544 (BCF02 (ESS)), 1543 (BCF01 (FAN)), 1546 (BCF07
 CC (MAN)), 1547 (BCF08 (NKO)) and 1545 (BCF03 (POC)). The sequence
 CC presented here is from the strain BCF02 (ESS) and corresponds to a
 CC fragment of the gp41 protein encoded by the env gene. The nucleic acids
 CC can be used to detect gp. O HIV-1 strains by hybridisation or (as
 CC primers) by gene amplification, also for screening and typing of such
 CC strains. Peptides encoded by the nucleic acids can be used as immunogens
 CC to raise Ab for detecting gp. O HIV-1.
 CC
 XX
 SQ Sequence 40 AA:
 SQ
 Query Match 75.7%; Score 131; DB 17; Length 40;
 Best Local Similarity 75.0%; Pred. No. 1e-11;
 Matches 21; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
 QY 3 ETLMDODORLNSGCKGRITCYTSARWH 30
 DB 11 etllqngqllnswgckgrivcytsvkn 38
 XX
 RESULT 13
 AAM80469
 ID AAM80469 standard; peptide: 32 AA.
 XX
 AC AAM80469;
 XX
 DT 28-JAN-1999 (first entry)
 XX
 DE Peptide derived from a conserved sequence of group O human HIV.
 XX
 KM Group O human immune deficiency virus; HIV; detection; infection.
 XX
 OS Synthetic.
 OS Immune deficiency virus.
 XX
 PN W09845323-A1.
 PD 15-OCT-1998.
 XX
 PF 06-APR-1998; 98WO-FR00691.
 XX
 PR 24-FEB-1998; 98FR-0002212.
 PR 09-APR-1997; 97FR-0004356.
 XX

CC a HIV envelope protein, and so the present sequence may be used as an
CC antigen for the detection of antibodies produced in response to HIV
infection.

XX Sequence 23 AA;

Query Match

Best Local Similarity 77.5%; Score 134; DB 21; Length 23;
Matches 22; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 8 DOORLNSWCGKGRITCYTSARWH 30
1 egqrlnswgckgrilicytsarwh 23

RESULT 9
AAB12254
ID AAB12254 standard; peptide: 23 AA.

AC AAB12254;

DT 10-NOV-2000 (first entry)

DE HIV-1 gp41 immunodominant region consensus sequence peptide 147 # 1.

KM HIV-1; AIDS; human immunodeficiency virus type 1; antibody detection;
KW acquired immunodeficiency syndrome; group O HIV; gp41.

OS Human immunodeficiency virus type 1.

PN EP1013766-A2.

PD 28-JUN-2000.

PF 29-NOV-1999; 99EP-0309491.

PR 30-NOV-1998; 98US-0110292.

PR 08-FEB-1999; 99US-0119138.

PR 04-NOV-1999; 99US-0433428.

PA (ORTH-) ORTHO-CLINICAL DIAGNOSTICS INC.

PI De Leys R, Zheng J;

DR WPI: 2000-402205/35.

XX New antigenic peptides and peptide functional derivatives, useful for
PT detection of antibodies produced in response to human immunodeficiency
PI virus group O antibodies -

PS Claim 1; Page 35; 52pp; English.

XX The present sequence is peptide 147 of Human Immunodeficiency Virus Type
CC 1 (HIV-1). This sequence is a partial consensus sequence of the
CC immunodominant region of gp41 protein derived from a variety of HIV-1
CC group O (outlier) strains: AN770, WVP5180, VAD, DUR, POC, FAN, LOB, MAN,
CC NAN, ESS, NKO, BCF09, BCF12, BCF13, BCF14, 686, ABT063, ABT124, ABT1123,
CC ABT2156, 193Ha, CDC7755, CDC1897, HLD28, 1515, 1516, D47-2d, HCYT2c,
CC Nt42 and PE41 (see AAB12207 to AAB12236). HIV is the principle
CC aetiological agent for acquired immunodeficiency syndrome (AIDS). gp41 is
CC a HIV envelope protein, and so the present sequence may be used as an
CC antigen for the detection of antibodies produced in response to HIV
CC infection.

XX Sequence 23 AA;

Query Match 76.9%; Score 133; DB 21; Length 23;
Best Local Similarity 95.7%; Pred. No. 2.9e-12;
Matches 22; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 8 DOORLNSWCGKGRITCYTSARWH 30

DB :|||||
1 egqrlnswgckgrilicytsarwh 23

RESULT 10
AAB12255
ID AAB12255 standard; peptide: 23 AA.

AC AAB12255;

DT 10-NOV-2000 (first entry)

DE HIV-1 gp41 immunodominant region consensus sequence peptide 147 # 2.

KM HIV-1; AIDS; human immunodeficiency virus type 1; antibody detection;
KW acquired immunodeficiency syndrome; group O HIV; gp41.

OS Human immunodeficiency virus type 1.

PN EP1013766-A2.

PD 28-JUN-2000. /note= "Any natural amino acid apart from L-asparagine"

PF 29-NOV-1999; 99EP-0309491.

PR 30-NOV-1998; 98US-0110292.

PR 08-FEB-1999; 99US-0119138.

PR 04-NOV-1999; 99US-0433428.

PA (ORTH-) ORTHO-CLINICAL DIAGNOSTICS INC.

PI De Leys R, Zheng J;

DR WPI: 2000-402205/35.

XX New antigenic peptides and peptide functional derivatives, useful for
PT detection of antibodies produced in response to human immunodeficiency
PI virus group O antibodies -

PS Claim 1; Page 35; 52pp; English.

XX The present sequence is a peptide 147 related peptide from Human
CC Immunodeficiency Virus Type 1 (HIV-1). This sequence is a partial
CC consensus sequence of the immunodominant region of gp41 protein derived
CC from a variety of HIV-1 group O (outlier) strains: AN770, WVP5180, VAD,
CC DUR, POC, FAN, LOB, MAN, NAN, ESS, NKO, BCF09, BCF12, BCF13, BCF14, 686,
CC ABT063, ABT124, ABT1123, ABT2156, 193Ha, CDC7755, CDC1897, HLD28, 1515,
CC 1516, D47-2d, HCYT2c, Nt42 and PE41 (see AAB12207 to AAB12236). HIV is
CC the principle aetiological agent for acquired immunodeficiency syndrome
CC (AIDS). gp41 is a HIV envelope protein, and so the present sequence may
CC be used as an antigen for the detection of antibodies produced in
CC response to HIV infection.

XX Sequence 23 AA;

Query Match 76.3%; Score 132; DB 21; Length 23;
Best Local Similarity 100.0%; Pred. No. 4e-12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 DOORLNSWCGKGRITCYTSARWH 30
2 egqrlnswgckgrilicytsarwh 23

RESULT 11
AAB12236
ID AAB12236 standard; peptide: 33 AA.

XX (ORTH-) ORTHO-CLINICAL DIAGNOSTICS INC.
 PA De Leys R, Zheng J;
 PI WPI: 2000-402205/35.
 DR
 XX New antigenic peptides and peptide functional derivatives, useful for
 PT detection of antibodies produced in response to human immunodeficiency
 PS virus group O antibodies -
 PS Example 5: Fig 6; 52pp: English.
 XX Human Immunodeficiency Virus (HIV) is the principle aetiological
 CC agent for acquired immunodeficiency syndrome (AIDS). gp41 is a HIV
 CC envelope protein, and may be used as an antigen for the detection of
 CC antibodies produced in response to HIV infection. Mosaic gp41 proteins
 CC were constructed, in which the immunodominant region of group M HIV was
 CC replaced by the corresponding region from group O HIV. The mosaic gp41
 CC proteins would be useful as antigens, used in the detection of anti-group
 CC O HIV antibodies produced in response to HIV infection. The present
 CC sequence is a dihydrofolate reductase (DHFR) fusion protein of one such
 CC mosaic protein.
 XX Sequence 439 AA;
 SQ
 Query Match 90.8%; Score 157; DB 21; Length 439;
 Best Local Similarity 96.4%; Pred. No. 2.4e-14;
 Matches 27; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 OY 3 ETLMDQDRLNSWCKGRITCYTSARWH 30
 Db 240 etlmqngqrlnswgckgrilcycsarwh 267
 RESULT 7
 AAB12257
 ID AAB12257 standard; peptide: 28 AA.
 XX AAB12257:
 AC
 XX 10-NOV-2000 (first entry)
 DT
 XX HIV-1 gp41 immunodominant region consensus sequence peptide 147 # 3.
 DE
 XX HIV-1: AIDS: human immunodeficiency virus type 1; antibody detection;
 KM acquired immunodeficiency syndrome; group O HIV; gp41.
 KW
 XX Human immunodeficiency virus type 1.
 OS
 XX Key Location/Qualifiers
 FH Misc-difference 6 /note- "Any natural amino acid apart from L-asparagine"
 FT
 XX EPI013766-A2.
 PN
 XX 28-JUN-2000.
 PD
 XX 29-NOV-1999; 99EP-0309491.
 PE
 XX 30-NOV-1998; 98US-0110292.
 PR 08-FEB-1999; 99US-0119138.
 PR 04-NOV-1999; 99US-0433428.
 PA (ORTH-) ORTHO-CLINICAL DIAGNOSTICS INC.
 PI De Leys R, Zheng J;
 PI WPI: 2000-402205/35.
 DR New antigenic peptides and peptide functional derivatives, useful for
 PT detection of antibodies produced in response to human immunodeficiency

PT virus group O antibodies -
 XX
 XX Claim 1; Page 36; 52pp: English.
 PS
 XX The present sequence is a peptide 147 related peptide from Human
 CC Immunodeficiency Virus Type 1 (HIV-1). This sequence is a partial
 CC consensus sequence of the immunodominant region of gp41 protein derived
 CC from a variety of HIV-1 group O (outlier) strains: ANT70, WVP5180, VANU,
 CC DNR, POC, FAN, MAN, NAN, ESS, NKO, BCF09, BCF12, BCF13, BCF14, 686,
 CC ABR063, ABR124, ABR1123, ABR2156, 193Ha, CDC7755, CDC1897, HLD28, 1515,
 CC 1516, D47-2d, HCYT2c, NT42 and PB41 (see AAB12207 to AAB12236). HIV is
 CC the principle aetiological agent for acquired immunodeficiency syndrome
 CC (AIDS). gp41 is a HIV envelope protein, and so the present sequence may
 CC be used as an antigen for the detection of antibodies produced in
 CC response to HIV infection.
 XX Sequence 28 AA;
 SQ
 Query Match 89.6%; Score 155; DB 21; Length 28;
 Best Local Similarity 96.4%; Pred. No. 2.5e-15;
 Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 OY 3 ETLMDQDRLNSWCKGRITCYTSARWH 30
 Db 1 etlmqngqrlnswgckgrilcycsarwh 28
 RESULT 8
 AAB12256
 ID AAB12256 standard; peptide: 23 AA.
 XX AAB12256:
 AC
 XX 10-NOV-2000 (first entry)
 DT
 XX HIV-1 gp41 immunodominant region consensus sequence peptide 147-4.
 DE
 XX HIV-1: AIDS: human immunodeficiency virus type 1; antibody detection;
 KM acquired immunodeficiency syndrome; group O HIV; gp41.
 KW
 XX Human immunodeficiency virus type 1.
 OS
 XX EPI013766-A2.
 PN
 XX 28-JUN-2000.
 PD
 XX 29-NOV-1999; 99EP-0309491.
 PE
 XX 30-NOV-1998; 98US-0110292.
 PR 08-FEB-1999; 99US-0119138.
 PR 04-NOV-1999; 99US-0433428.
 PA (ORTH-) ORTHO-CLINICAL DIAGNOSTICS INC.
 PI De Leys R, Zheng J;
 PI WPI: 2000-402205/35.
 DR New antigenic peptides and peptide functional derivatives, useful for
 PT detection of antibodies produced in response to human immunodeficiency
 PS virus group O antibodies -
 PS Claim 1; Page 36; 52pp: English.
 XX The present sequence is peptide 147-4 from Human Immunodeficiency Virus
 CC Type 1 (HIV-1). This sequence is a partial consensus sequence of the
 CC immunodominant region of gp41 protein derived from a variety of HIV-1
 CC group O (outlier) strains: ANT70, WVP5180, VANU, DNR, POC, FAN, MAN,
 CC NAN, ESS, NKO, BCF09, BCF12, BCF13, BCF14, 686, ABR063, ABR1123,
 CC ABR2156, 193Ha, CDC7755, CDC1897, HLD28, 1515, D47-2d, HCYT2c,
 CC NT42 and PB41 (see AAB12207 to AAB12236). HIV is the principle
 CC aetiological agent for acquired immunodeficiency syndrome (AIDS). gp41 is

XX	RESULT	4
XX	AAB12261	
ID	AAB12261 standard; peptide; 220 AA.	
XX		
AC	AAB12261;	
XX		
DT	10-NOV-2000 (first entry)	
XX		
XX	HIV group M/ group O.mosaic protein # 1.	
KW	HIV-1; AIDS; human immunodeficiency virus type 1;	
KW	acquired immunodeficiency syndrome; group O HIV; gp41.	
XX		
OS	Human immunodeficiency virus type 1.	
XX		
PN	EPI013766-A2.	
PD	28-JUN-2000.	
XX		
PE	29-NOV-1999; 99EP-0309491.	
XX		
PR	30-NOV-1998; 98US-0110292.	
PR	08-FEB-1999; 99US-0119138.	
PR	-04-NOV-1999; 99US-0433428.	
XX		
PA	(ORTH-) ORTHO-CLINICAL DIAGNOSTICS INC.	
XX		
FI	De Lays R, Zheng J;	
DR	WPI; 2000-402205/35.	
XX		
PT	New antigenic peptides and peptide functional derivatives, useful for	
PT	detection of antibodies produced in response to human immunodeficiency	
PT	virus group O antibodies -	
PS		
PS	Claim 15; Page 37-38; 52pp; English.	
XX		
CC	Human Immunodeficiency Virus (HIV) is the principle aetiological	
CC	agent for acquired immunodeficiency syndrome (AIDS). gp41 is a HIV	
CC	envelope protein, and may be used as an antigen for the detection of	
CC	antibodies produced in response to HIV infection. Mosaic gp41 proteins	
CC	were constructed, in which the immunodominant region of group M HIV was	
CC	replaced by the corresponding region from group O HIV. The mosaic gp41	
CC	proteins would be useful as antigens, used in the detection of anti-group	
CC	O HIV antibodies produced in response to HIV infection. The present	
CC	sequence is one such mosaic protein.	
XX		
SQ	Sequence 220 AA;	
XX		
Query Match	90.8%; Score 157; DB 21; Length 220;	
Best Local Similarity	96.4%; Pred. NO.1.le-14;	
Matches 27; Conservative 1; Mismatches 0; Indels 0; Gaps 0		
OY	3 ETLIMODOORLNSMGCKGRITCYTSARWH 30	
	: : : :	
DB	44 etlmqngqlnswgckgritcytsarwh 71	
XX		
RESULT	5	
ID	AAB12253	
XX	AAB12253 standard; peptide; 368 AA.	
XX		
AC	AAB12253;	
XX		
DT	10-NOV-2000 (first entry)	
XX		
DE	DHFR-hes-MH fusion protein.	
XX		
KW	HIV-1; AIDS; human immunodeficiency virus type 1; DHFR-hes-MH;	
KW	acquired immunodeficiency syndrome; group O HIV; gp41.	
XX		

Query Match	Best Local Similarity	Score 157;	DB 21;	Length 368;
Matches 27; Conservative	96.4%;	Pred. No. 2e-14;	1; Mismatches 0;	Indels 0; Gaps 0
QY 3 ETLMDQQRHNSGCKGRITCTTSARWH 30	: : :			
Db 240 etlmgqgrlnsgckgrilcytsarwh 267				
RESULT 6				
AAB12252				
ID	AAB12252 standard; peptide; 439 AA.			
XX				
AC	AAB12252;			
XX				
DT	10-NOV-2000 (first entry)			
XX				
DE	DHFR-hENV-MH fusion protein.			
XX				
KW	HIV-1; AIDS; human immunodeficiency virus type 1; DHFR-hENV-MH;			
XX	acquired immunodeficiency syndrome; group O HIV; gp41.			
OS	Human immunodeficiency virus type 1.			
XX	unidentified.			
PN	EPI1013766-A2.			
PD	28-JUN-2000.			
XX				
PE	29-NOV-1999; 99EP-0309491.			
XX				
PI	De Lays R, Zheng J;			
DR	WPI, 2000-402205/35.			
XX				
PT	New antigenic peptides and peptide functional derivatives; useful for			
PT	detection of antibodies produced in response to human immunodeficiency			
PT	virus group O antibodies -			
XX				
PS	Example 5; Fig 6; 52pp; English.			
XX				
CC	Human Immunodeficiency Virus (HIV) is the principle aetiological			
CC	agent for acquired immunodeficiency syndrome (AIDS). gp41 is a HIV			
CC	envelope protein, and may be used as an antigen for the detection of			
CC	antibodies produced in response to HIV infection. Mosaic gp41 proteins			
CC	were constructed, in which the immunodominant region of group M HIV was			
CC	replaced by the corresponding region from group O HIV. The mosaic gp41			
CC	proteins would be useful as antigens, used in the detection of anti-group			
CC	O HIV antibodies produced in response to HIV infection. The present			
CC	sequence is a dithydrifolate reductase (DHFR) fusion protein of one such			
XX	mosaic protein.			
SQ	Sequence 368 AA;			

XX Claim 1; Page 36; 52pp; English.

PS The present sequence is peptide 147-5 from Human Immunodeficiency Virus

CC Type 1 (HIV-1). This sequence is a partial consensus sequence of the

CC immunodominant region of gp41 protein derived from a variety of HIV-1

CC group O (outlier) strains: AN770, MWP5180, VAV, DOR, POC, FAN, LOB, MAN,

CC NAN, ESS, NKO, BCF09, BCF12, BCF13, BCF14, 686, ABT063, ABT124, ABT1123,

CC ABT2156, 193He, CDC7755, CDC1897, HLD28, 1515, 1516, D47-2d, HCVT2c,

CC Nr42 and Pe41 (see AAB12207 to AAB12236). HIV is the principle

CC aetiological agent for acquired immunodeficiency syndrome (AIDS). gp41 is

CC a HIV envelope protein, and so the present sequence may be used as an

CC antigen for the detection of antibodies produced in response to HIV

CC infection.

XX

SQ -Sequence 30 AA:

Query Match 100.0%; Score 173; DB 21; Length 30;

Best Local Similarity 100.0%; Pred. No. 6.9e-18;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRETLMQDQRLNSWCGKGRITCYTSARWH 30

|||||:|||||:|||||:|||||:|||||

Db 1 gretlmqdgqlnswcgkgrilicytsarwh 30

RESULT 2

AAB12259

ID AAB12259 standard; peptide: 35 AA.

XX AAB12259;

XX 10-NOV-2000 (first entry)

DE Group O HIV-1 gp41 replacement peptide # 1.

XX

XX HIV-1: AIDS: human immunodeficiency virus type 1; antibody detection;

KW acquired immunodeficiency syndrome; group O HIV; gp41.

XX

OS Human immunodeficiency virus type 1.

XX

PN EPI013766-A2.

PD 28-JUN-2000.

XX

XX 29-NOV-1999; 99EP-0309491.

PF

XX 30-NOV-1998; 98US-0110292.

PR

XX 08-FEB-1999; 99US-0119138.

PR

XX 04-NOV-1999; 99US-0433428.

XX

PA (ORTH-) ORTHO-CLINICAL DIAGNOSTICS INC.

XX

PI De Leys R, Zheng J;

PI

XX WPI; 2000-402205/35.

DR

XX

XX New antigenic peptides and peptide functional derivatives, useful for

PT detection of antibodies produced in response to human immunodeficiency

PT virus group O antibodies -

XX

XX

PS Claim 1; Page 37; 52pp; English.

XX

XX The present sequence is a group O Human Immunodeficiency Virus Type 1

CC (HIV-1) gp41 peptide. HIV is the principle aetiological agent for

CC acquired immunodeficiency syndrome (AIDS). gp41 is a HIV envelope

CC protein. The present sequence was derived from a sequence homology

CC alignment of group O and group M HIV gp41 descending helix sequences.

CC The present sequence was used as a group O replacement peptide, where it

CC was used to construct mosaic gp41 proteins, in which the group M

CC immunodominant region was replaced by the present sequence. The mosaic

CC gp41 proteins (AAB12261 and AAB12262) would be useful as antigens, which

CC would be used for the detection of anti-group O HIV antibodies produced

CC in response to HIV infection.

XX

SQ Sequence 35 AA:

Query Match 90.8%; Score 157; DB 21; Length 35;

Best Local Similarity 96.4%; Pred. No. 1.6e-15;

Matches 27; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 ETLMQDQRLNSWCGKGRITCYTSARWH 30

|||||:|||||:|||||:|||||:|||||

Db 8 etlmqngqrlnswcgkgrilicytsarwh 35

RESULT 3

AAB12262

ID AAB12262 standard; peptide: 149 AA.

XX AAB12262;

XX 10-NOV-2000 (first entry)

DE HIV group M/ group O mosaic protein # 2.

XX

XX HIV-1: AIDS: human immunodeficiency virus type 1;

KW acquired immunodeficiency syndrome; group O HIV; gp41.

XX

OS Human immunodeficiency virus type 1.

XX

PN EPI013766-A2.

PD 28-JUN-2000.

XX

XX 29-NOV-1999; 99EP-0309491.

PF

XX 30-NOV-1998; 98US-0110292.

PR

XX 08-FEB-1999; 99US-0119138.

PR

XX 04-NOV-1999; 99US-0433428.

XX

PA (ORTH-) ORTHO-CLINICAL DIAGNOSTICS INC.

XX

PI De Leys R, Zheng J;

PI

XX WPI; 2000-402205/35.

DR

XX

XX New antigenic peptides and peptide functional derivatives, useful for

PT detection of antibodies produced in response to human immunodeficiency

PT virus group O antibodies -

XX

XX

PS Claim 15; Page 38-39; 52pp; English.

XX

XX Human Immunodeficiency Virus (HIV) is the principle aetiological

CC agent for acquired immunodeficiency syndrome (AIDS). gp41 is a HIV

CC envelope protein, and may be used as an antigen for the detection of

CC antibodies produced in response to HIV infection. Mosaic gp41 proteins

CC were constructed, in which the immunodominant region of group M HIV was

CC replaced by the corresponding region from group O HIV. The mosaic gp41

CC proteins would be useful as antigens, used in the detection of anti-group

CC O HIV antibodies produced in response to HIV infection. The present

CC sequence is one such mosaic protein.

XX

SQ Sequence 149 AA:

Query Match 90.8%; Score 157; DB 21; Length 149;

Best Local Similarity 96.4%; Pred. No. 7.5e-15;

Matches 27; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 ETLMQDQRLNSWCGKGRITCYTSARWH 30

|||||:|||||:|||||:|||||:|||||

Db 44 etlmqngqrlnswcgkgrilicytsarwh 71

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 20, 2002, 15:26:17 ; Search time 29.93 Seconds

(Without alignments)
111.334 Million cell updates/sec

Title: US-09-605-573A-69

Perfect score: 173

Sequence: 1 GRETLMQDOORLNSWCKGRICYSARWH 30

Scoring table: BLOSUM62

Gapop 10.0 , Gapect 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT:*
2: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT:*
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7: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1986.DAT:*
8: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1987.DAT:*
9: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1988.DAT:*
10: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1989.DAT:*
11: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1990.DAT:*
12: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1991.DAT:*
13: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1992.DAT:*
14: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1993.DAT:*
15: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1994.DAT:*
16: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1995.DAT:*
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18: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1997.DAT:*
19: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT:*
20: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT:*
21: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT:*
22: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	173	100.0	30	21	AA12264
2	157	90.8	35	21	AA12259
3	157	90.8	149	21	AA12262
4	157	90.8	220	21	AA12261
5	157	90.8	368	21	AA12253
6	157	90.8	439	21	AA12252
7	155	89.6	28	21	AA12257
8	134	77.5	23	21	AA12256
9	133	76.9	23	21	AA12254
10	132	76.3	23	21	AA12255
11	131	75.7	33	21	AA12236

12	131	75.7	40	17	AA07343	Partial sequence o
13	130	75.1	32	19	AA080469	Peptide derived fr
14	130	75.1	33	21	AA12229	Partial sequence o
15	130	75.1	36	21	AA167606	Peptide #6 for det
16	130	75.1	113	20	AA105554	HIV-1 group O Isol
17	129	74.6	33	21	AA12231	Partial sequence o
18	129	74.6	40	17	AA07346	Partial sequence o
19	128	74.0	33	21	AA12208	Partial sequence o
20	128	74.0	33	21	AA12215	Partial sequence o
21	128	74.0	33	21	AA12216	Partial sequence o
22	128	74.0	33	21	AA12218	Partial sequence o
23	128	74.0	33	21	AA12219	Partial sequence o
24	128	74.0	35	15	AA151690	HIV isolate WVP-51
25	128	74.0	35	20	AA03073	HIV isolate WVP-51
26	128	74.0	36	21	AA131617	Peptide #7 for det
27	128	74.0	36	21	AA167607	HIV gp41 antigen p
28	128	74.0	36	21	AA155784	Anti-HIV-1 group O
29	128	74.0	36	22	AA162574	SEQ ID NO. 105 fro
30	128	74.0	167	19	AA169320	HIV isolate WVP-51
31	128	74.0	204	19	AA122909	HIV isolate WVP-51
32	128	74.0	351	15	AA151687	Human Immunodefici
33	128	74.0	351	15	AA151687	Human Immunodefici
34	127	73.4	33	22	AA12212	Partial sequence o
35	127	73.4	33	20	AA130515	Allelic peptide fo
36	127	73.4	36	21	AA179777	HIV detection rela
37	127	73.4	36	21	AA167613	Peptide #13 for de
38	127	73.4	36	21	AA167615	Peptide #15 for de
39	127	73.4	36	21	AA167615	HIV (Group O) pept
40	127	73.4	36	21	AA167615	Peptide antigen cr
41	127	73.4	36	22	AA162597	Partial sequence o
42	127	73.4	36	22	AA162597	Partial sequence o
43	127	73.4	111	20	AA105561	HIV-1 group O Isol
44	126	72.8	33	21	AA12230	Partial sequence o
45	126	72.8	40	17	AA07345	Partial sequence o

ALIGNMENTS

RESULT 1	AA12264	standard; peptide: 30 AA.
ID	AA12264	
XX	AA12264	
AC	AA12264	
XX	AA12264	
DT	10-NOV-2000	(first entry)
XX	10-NOV-2000	
DE	HIV-1 gp41 immunodominant region consensus sequence peptide 147-5.	
XX	HIV-1; AIDS; human immunodeficiency virus type 1; antibody detection;	
KW	acquired immunodeficiency syndrome; group O HIV; gp41.	
XX	Human immunodeficiency virus type 1.	
OS	Human immunodeficiency virus type 1.	
XX	EP1013766-A2.	
PN	EP1013766-A2.	
XX	28-JUN-2000.	
PD	28-JUN-2000.	
XX	29-NOV-1999.	99EP-0309491.
PF	29-NOV-1999.	99EP-0309491.
XX	30-NOV-1998.	98US-0110292.
PR	08-FEB-1999.	99US-0119138.
PR	04-NOV-1999.	99US-0433428.
XX	(ORTH-) ORTHO-CLINICAL DIAGNOSTICS INC.	
PA	De Leys R, Zheng J;	
XX	De Leys R, Zheng J;	
PI	WPI; 2000-402205/35.	
XX	WPI; 2000-402205/35.	
DR	New antigenic peptides and peptide functional derivatives, useful for	
XX	detection of antibodies produced in response to human immunodeficiency	
PT	virus group O antibodies -	
PT	virus group O antibodies -	

PA (SNFI) PASTEUR SANOCS SA.
 XX Chenebaux DMB, Delagneau H, Gadelles SJX, Rleunier FY;
 XX WPI: 1998-583190/49.
 DR
 XX New synthetic peptide(s) - useful for, e.g. detecting infection by
 PT human immune deficiency virus of group O
 XX
 PS Claim 6; Page 44; 55pp; French.
 XX
 CC AAN80459-74 represent synthetic peptides (either linear or cyclised by
 CC Cys-Cys disulphide bonds). The peptides represent variable sequences
 CC connected around short highly conserved sequences present in isolates
 CC of group O human immune deficiency virus (HIV). The peptides are
 CC useful as immunological reagents for detecting infection by group O
 CC human immune deficiency virus (HIV).
 CC
 SQ Sequence 32 AA;

Query Match 75.1%; Score 130; DB 19; Length 32;
 Best Local Similarity 71.4%; Pred. No. 1,1e-11;
 Matches 20; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

OY 3 ETLMDQORLNSMGCKGRITCYTSARWH 30
 ||||:||||:||||:||||:|
 Db 3 etllmqnqlnswgcgrtlvcysvrvwn 30

RESULT 14

AAB12229
 ID AAB12229 standard; peptide: 33 AA.

AC AAB12229;

DT 10-NOV-2000 (first entry)

DE Partial sequence of HIV-1 strain HLD28 gp41 immunodominant region.

KW HIV-1; AIDS; human immunodeficiency virus type 1; immunodominant region;
 acquired immunodeficiency syndrome; group O HIV; gp41; HLD28.

OS Human immunodeficiency virus type 1.

XX EP1013766-A2.

PD 28-JUN-2000.

PF 29-NOV-1999; 99EP-0309491.

PR 30-NOV-1998; 98US-0110292.

PR 08-FEB-1999; 99US-0119136.

PR 04-NOV-1999; 99US-0433428.

PA (ORTH-) ORTHO-CLINICAL DIAGNOSTICS INC.

XX De Leys R, Zheng J;

DR WPI: 2000-402205/35.

PT New antigenic peptides and peptide functional derivatives, useful for
 PT detection of antibodies produced in response to human immunodeficiency
 PT virus group O antibodies -

XX Example 1; Fig 1; 52pp; English.

CC The present sequence is a partial gp41 protein of Human Immunodeficiency
 CC Virus Type 1 (HIV-1) strain HLD28. HIV is the principle aetiological
 CC agent for acquired immunodeficiency syndrome (AIDS). gp41 is a HIV
 CC envelope protein, and may be used as an antigen for the detection of
 CC antibodies produced in response to HIV infection. HLD28 is a member of
 CC HIV group O (outlier). The present sequence is the immunodominant region

CC of gp41. This sequence was used in a sequence homology alignment,
 CC which in turn was used to derive a consensus sequence peptide: peptide
 CC 147 (AAB12254).
 CC
 SQ Sequence 33 AA;

Query Match 75.1%; Score 130; DB 21; Length 33;
 Best Local Similarity 75.0%; Pred. No. 1,1e-11;
 Matches 21; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 3 ETLMDQORLNSMGCKGRITCYTSARWH 30
 ||||:||||:||||:||||:|
 Db 6 etllmqnqrlidwgcgrtlvcysvrvwn 33

RESULT 15

AAV67606
 ID AAV67606 standard; peptide: 36 AA.

AC AAV67606;

DT 23-MAR-2000 (first entry)

DE Peptide #6 for detecting HIV-1 group O infection.

KW Human immunodeficiency virus-1; HIV-1; gp41 envelope protein; detection;
 increased structural stability; diagnostic antigen.

OS Synthetic.

PN WO962945-A2.

PD 09-DEC-1999.

PF 04-JUN-1999; 99WO-US12446.

PR 05-JUN-1998; 98US-0088229.

PR 01-SEP-1998; 98US-0098705.

PR 15-SEP-1998; 98US-0100422.

PR 28-JAN-1999; 99WO-US01726.

PA (PEPT-) PEPTIDE SOLUTIONS INC.

XX Chowdhury MA, Bernstein D, Molsenbocker MA;

DR WPI: 2000-086953/07.

PT Improving properties of peptides for use as diagnostic antigens or for
 PT preventing or treating infections -

XX Claim 18; Page 61; 83pp; English.

CC This peptide is derived from the human immunodeficiency virus (HIV)-1
 CC gp41 envelope protein, and is useful for detecting HIV-1 group O
 CC infection. The invention relates to peptides derived from HIV-1 which
 CC have been modified for use as diagnostic antigens in the treatment or
 CC prevention of infection. The structural stability of the peptides can be
 CC increased in four different ways: through the replacement of a
 CC hydrophobic amino acid with a less hydrophobic amino acid; through an
 CC increase in the amount of secondary structure (i.e. alpha helix) in the
 CC peptide; through the removal of a positive charge from the peptide; or
 CC through the constraint of the epitopic sequence from the formation of a
 CC covalent crosslink. Modified peptides of the invention are used to detect
 CC infectious agents specifically HIV-1. Other detectable agents include
 CC Group O viruses; human T-cell lymphotropic virus-I or -II; hepatitis C
 CC and the causative agent of syphilis. The peptides can be used for
 CC prevention or treatment of infections (e.g. as vaccines, or where
 CC expressed from a transgene). More generally almost any peptide can be
 CC similarly modified, e.g. cytokines and interferons; major
 CC histocompatibility complex antigens; hormones; growth factors; tumour
 CC markers or suppressors, or antigens from many other pathogens.

Sequence 36 AA;

Query Match 75.1%; Score 130; DB 21; Length 36;
 Best Local Similarity 75.0%; Pred. No. 1.3e-11;
 Matches 21; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 3 ETLMDODORLNSGCKGRRIICYTSARWH 30
 |||:||||| |||||:||||| :||
 Db 8 etllqngqrlnlwgcgkgrllcyltslkn 35

Search completed: June 20, 2002, 15:31:31
 Job time: 314 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 20, 2002, 15:28:12 ; Search time 12.97 Seconds

(without alignments)
56.497 Million cell updates/sec

Title: US-09-605-573A-69

Perfect score: 173

Sequence: 1 GRETLMODQORLNSMCKGRITCYTSARWH 30

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents, AA: *
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2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
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4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/6C.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/Backfiles1.pep:*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	173	100.0	30	4	US-09-433-428D-69
2	166	96.0	30	4	US-09-433-428D-63
3	157	90.8	149	4	US-09-433-428D-67
4	157	90.8	220	4	US-09-433-428D-66
5	157	90.8	368	4	US-09-433-428D-58
6	157	90.8	439	4	US-09-433-428D-57
7	155	89.6	28	4	US-09-433-428D-62
8	155	89.6	35	4	US-09-433-428D-64
9	134	77.5	23	4	US-09-433-428D-61
10	133	76.9	23	4	US-09-433-428D-59
11	132	76.3	23	4	US-09-433-428D-60
12	131	75.7	33	4	US-09-433-428D-30
13	131	75.7	40	3	US-08-894-699-36
14	131	75.7	40	4	US-09-444-410-36
15	130	75.1	33	4	US-09-433-428D-23
16	129	74.6	33	4	US-09-433-428D-25
17	129	74.6	40	3	US-08-894-699-39
18	129	74.6	40	4	US-09-444-410-39
19	128	74.0	33	4	US-09-433-428D-2
20	128	74.0	33	4	US-09-433-428D-9
21	128	74.0	33	4	US-09-433-428D-10
22	128	74.0	33	4	US-09-433-428D-12
23	128	74.0	33	4	US-09-433-428D-13
24	128	74.0	35	1	US-08-470-202-62
25	128	74.0	35	1	US-08-471-770-62
26	128	74.0	35	2	US-08-468-059-62
27	128	74.0	35	4	US-09-109-916-62

28	128	74.0	146	2	US-08-394-021-10	Sequence 10, Appl
29	128	74.0	146	4	US-09-131-551-10	Sequence 10, Appl
30	128	74.0	204	4	US-08-965-056-105	Sequence 105, Appl
31	128	74.0	351	1	US-08-470-202-46	Sequence 46, Appl
32	128	74.0	351	1	US-08-471-770-46	Sequence 46, Appl
33	128	74.0	351	2	US-08-468-059-46	Sequence 46, Appl
34	128	74.0	351	4	US-09-109-916-46	Sequence 46, Appl
35	127	73.4	33	4	US-09-433-428D-6	Sequence 6, Appl
36	127	73.4	40	3	US-08-894-699-68	Sequence 68, Appl
37	127	73.4	40	4	US-09-444-410-68	Sequence 68, Appl
38	126	72.8	33	4	US-09-433-428D-24	Sequence 24, Appl
39	126	72.8	40	3	US-08-894-699-38	Sequence 38, Appl
40	126	72.8	40	4	US-09-444-410-38	Sequence 38, Appl
41	125	72.3	33	4	US-09-433-428D-20	Sequence 20, Appl
42	125	72.3	40	3	US-08-894-699-41	Sequence 41, Appl
43	125	72.3	40	4	US-09-444-410-41	Sequence 41, Appl
44	125	72.3	356	1	US-08-602-713-12	Sequence 12, Appl
45	125	72.3	356	4	US-08-989-493-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-09-433-428D-69; Sequence 69, Application US/09433428D
; Patent No. 6149910

Query Match 100.0%; Score 173; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.2e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRETLMODQORLNSMCKGRITCYTSARWH 30
DB 1 GRETLMODQORLNSMCKGRITCYTSARWH 30

RESULT 2
US-09-433-428D-63
; Sequence 63, Application US/09433428D
; Patent No. 6149910
; GENERAL INFORMATION:
; APPLICANT: De leys, Robert J.
; TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
; FILE REFERENCE: CDS-207
; CURRENT APPLICATION NUMBER: US/09/433,428D
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 63
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

RESULT 7
US-09-433-428D-62

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Sequence 62, Application US/09433428D
Patent No. 6149910
GENERAL INFORMATION:
APPLICANT: De Leys, Robert J.
APPLICANT: Zheng, Jian
TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
FILE REFERENCE: CDS-207
CURRENT APPLICATION NUMBER: US/09/433,428D
CURRENT FILING DATE: 1999-11-04
NUMBER OF SEQ ID NOS: 70
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 62
LENGTH: 28
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: Xaa is any amino acid
LOCATION: 6
OTHER INFORMATION: Description of Artificial Sequence:HIV Consensus
OTHER INFORMATION: Sequence
US-09-433-428D-62
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Query Match          89.6%; Score 155; DB 4; Length 28;
Best Local Similarity 96.4%; Pred. No. 1e-16;
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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OY 3 ETLMDODORLNSMCGCKGRITCYTSARWH 30
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DB 1 ETLMDODORLNSMCGCKGRITCYTSARWH 28
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```
RESULT 8
US-09-433-428D-64
Sequence 64, Application US/09433428D
Patent No. 6149910
GENERAL INFORMATION:
APPLICANT: De Leys, Robert J.
APPLICANT: Zheng, Jian
TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
FILE REFERENCE: CDS-207
CURRENT APPLICATION NUMBER: US/09/433,428D
CURRENT FILING DATE: 1999-11-04
NUMBER OF SEQ ID NOS: 70
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 64
LENGTH: 35
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: Xaa is any amino acid
LOCATION: 13
OTHER INFORMATION: Description of Artificial Sequence:HIV Consensus
OTHER INFORMATION: Sequence
US-09-433-428D-64
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```
Query Match          89.6%; Score 155; DB 4; Length 35;
Best Local Similarity 96.4%; Pred. No. 1.3e-16;
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
OY 3 ETLMDODORLNSMCGCKGRITCYTSARWH 30
    ||||| ||||| ||||| ||||| |||||
DB 8 ETLMDODORLNSMCGCKGRITCYTSARWH 35
```

```
RESULT 9
US-09-433-428D-61
Sequence 61, Application US/09433428D
Patent No. 6149910
GENERAL INFORMATION:
APPLICANT: De Leys, Robert J.
APPLICANT: Zheng, Jian
```

```
TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
FILE REFERENCE: CDS-207
CURRENT APPLICATION NUMBER: US/09/433,428D
CURRENT FILING DATE: 1999-11-04
NUMBER OF SEQ ID NOS: 70
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 61
LENGTH: 23
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:HIV Consensus
OTHER INFORMATION: Sequence
US-09-433-428D-61
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Query Match          77.5%; Score 134; DB 4; Length 23;
Best Local Similarity 95.7%; Pred. No. 1.1e-13;
Matches 22; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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OY 8 DQORLNSMCGCKGRITCYTSARWH 30
    :|||: ||||| ||||| ||||| |||||
DB 1 EQORLNSMCGCKGRITCYTSARWH 23
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```
RESULT 10
US-09-433-428D-59
Sequence 59, Application US/09433428D
Patent No. 6149910
GENERAL INFORMATION:
APPLICANT: De Leys, Robert J.
APPLICANT: Zheng, Jian
TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
FILE REFERENCE: CDS-207
CURRENT APPLICATION NUMBER: US/09/433,428D
CURRENT FILING DATE: 1999-11-04
NUMBER OF SEQ ID NOS: 70
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 59
LENGTH: 23
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:HIV Consensus
OTHER INFORMATION: Sequence
US-09-433-428D-59
```

```
Query Match          76.9%; Score 133; DB 4; Length 23;
Best Local Similarity 95.7%; Pred. No. 1.6e-13;
Matches 22; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 8 DQORLNSMCGCKGRITCYTSARWH 30
    :|||: ||||| ||||| ||||| |||||
DB 1 NOORLNSMCGCKGRITCYTSARWH 23
```

```
RESULT 11
US-09-433-428D-60
Sequence 60, Application US/09433428D
Patent No. 6149910
GENERAL INFORMATION:
APPLICANT: De Leys, Robert J.
APPLICANT: Zheng, Jian
TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
FILE REFERENCE: CDS-207
CURRENT APPLICATION NUMBER: US/09/433,428D
CURRENT FILING DATE: 1999-11-04
NUMBER OF SEQ ID NOS: 70
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 60
LENGTH: 23
TYPE: PRT
```

```

; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Xaa is any amino acid
; LOCATION: 1
; OTHER INFORMATION: Description of Artificial Sequence: HIV Consensus
US-09-433-428D-60

```

```

Query Match
Best Local Similarity 76.3%; Score 132; DB 4; Length 23;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

; Y 9 QOHLNSWGCKGRICVTSARWH 30
; 2 QOHLNSWGCKGRICVTSARWH 23

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RESULT 12

```

US-09-433-428D-30
; Sequence 30, Application US/09433428D
; Patent No. 6149910
; GENERAL INFORMATION:
; APPLICANT: De Leys, Robert J.
; APPLICANT: Zheng, Jian
; TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
; FILE REFERENCE: CDS-207
; CURRENT APPLICATION NUMBER: US/09/433,428D
; CURRENT FILING DATE: 1999-11-04
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-433-428D-30

```

```

Query Match
Best Local Similarity 75.7%; Score 131; DB 4; Length 33;
Matches 21; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

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```

; Y 3 ETLMDQORLNSWGCKGRICVTSARWH 30
; 6 ETLMDQORLNSWGCKGRICVTSARWH 33

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RESULT 13

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US-08-894-699-36
; Sequence 36, Application US/08894699
; Patent No. 6030769
; GENERAL INFORMATION:
; APPLICANT: SIMON, FRANCOIS
; APPLICANT: SARAGOSTI, SENTOB
; APPLICANT: LOUSSEY-ATAKA, IBITISSAM
; APPLICANT: LY, THOI-DUONG
; APPLICANT: CHAIX-BAUDIER, MARIE-LAURE
; TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MATER & NEUSTADT,
; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/894,699
; FILING DATE: 01-DEC-1997
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR96/00294
; FILING DATE: 26-FEB-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 95/02236
; FILING DATE: 27-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,614
; REFERENCE/DOCKET NUMBER: 0354-0020-0PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-894-699-36

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Query Match
Best Local Similarity 75.7%; Score 131; DB 3; Length 40;
Matches 21; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

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; Y 3 ETLMDQORLNSWGCKGRICVTSARWH 30
; 11 ETLMDQORLNSWGCKGRICVTSARWH 38

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RESULT 14

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US-09-444-410-36
; Sequence 36, Application US/09444410
; Patent No. 6270975
; GENERAL INFORMATION:
; APPLICANT: SIMON, FRANCOIS
; APPLICANT: SARAGOSTI, SENTOB
; APPLICANT: LOUSSEY-ATAKA, IBITISSAM
; APPLICANT: LY, THOI-DUONG
; APPLICANT: CHAIX-BAUDIER, MARIE-LAURE
; TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MATER & NEUSTADT,
; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/444,410
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/894,699
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 95/02236

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FILING DATE: 27-FEB-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: OBLON, NORMAN F.
 REGISTRATION NUMBER: 24,614
 REFERENCE/DOCKET NUMBER: 0354-0020-0PCT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 703-413-3000
 TELEFAX: 703-413-2220
 INFORMATION FOR SEQ ID NO: 36:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 40 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-09-444-410-36

Query Match 75.7%; Score 131; DB 4; Length 40;
 Best Local Similarity 75.0%; Pred. No. 5.7e-13;
 Matches 21; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 3 ETLMDODRLNSMGCKGRITCYTSARWH 30
 |||:|||||:|||||:|||||:|:
 Db 11 ETLIONOOLNSMGCKGRIVCYTSYKWN 38

RESULT 15
 US-09-433-428D-23
 : Sequence 23, Application US/09433428D
 : Patent No. 6149910
 : GENERAL INFORMATION:
 : APPLICANT: De Leys, Robert J.
 : TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
 : FILE REFERENCE: CDS-207
 : CURRENT APPLICATION NUMBER: US/09/433,428D
 : CURRENT FILING DATE: 1999-11-04
 : NUMBER OF SEQ ID NOS: 70
 : SOFTWARE: Patentin Ver. 2.0
 : SEQ ID NO 23
 : LENGTH: 33
 : TYPE: PRT
 : ORGANISM: Human Immunodeficiency virus type 1
 : US-09-433-428D-23

Query Match 75.1%; Score 130; DB 4; Length 33;
 Best Local Similarity 75.0%; Pred. No. 6.5e-13;
 Matches 21; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 3 ETLMDODRLNSMGCKGRITCYTSARWH 30
 |||:|||||:|||||:|||||:|:
 Db 6 ETLMDODRLNSMGCKGRITCYTSYKWN 33

Search completed: June 20, 2002, 15:31:50
 Job time: 218 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 20, 2002, 15:30:32 ; Search time 105.35 Seconds

(without alignments)
100.232 Million cell updates/sec

Title: US-09-605-573a-69

Perfect score: 173
Sequence: 1 GRETLMODODRLNSWCKGRICITSARWH 30Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3502263 seqs, 351980561 residues

Total number of hits satisfying chosen parameters: 3502263

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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16: /cgn2_6/ptodata/2/paa/US092_COMB.pep:*
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26: /cgn2_6/ptodata/2/paa/US60_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	173	100.0	30	18	US-09-433-428-69
2	173	100.0	30	20	US-09-605-573a-69
3	166	96.0	30	18	US-09-433-428-63
4	166	96.0	30	20	US-09-605-573a-63
5	157	90.8	149	18	US-09-433-428-67
6	157	90.8	149	20	US-09-605-573a-67
7	157	90.8	220	18	US-09-433-428-66

	8	157	90.8	220	20	US-09-605-573a-66	Sequence 66, Appl
	9	157	90.8 <td>368</td> <td>18</td> <td>US-09-433-428-58</td> <td>Sequence 58, Appl</td>	368	18	US-09-433-428-58	Sequence 58, Appl
	10	157	90.8 <td>368</td> <td>20</td> <td>US-09-605-573a-58</td> <td>Sequence 58, Appl</td>	368	20	US-09-605-573a-58	Sequence 58, Appl
	11	157	90.8 <td>439</td> <td>18</td> <td>US-09-433-428-57</td> <td>Sequence 57, Appl</td>	439	18	US-09-433-428-57	Sequence 57, Appl
	12	157	90.8 <td>439</td> <td>20</td> <td>US-09-605-573a-57</td> <td>Sequence 57, Appl</td>	439	20	US-09-605-573a-57	Sequence 57, Appl
	13	155	89.6 <td>28</td> <td>18</td> <td>US-09-433-428-62</td> <td>Sequence 62, Appl</td>	28	18	US-09-433-428-62	Sequence 62, Appl
	14	155	89.6 <td>28</td> <td>20</td> <td>US-09-605-573a-62</td> <td>Sequence 62, Appl</td>	28	20	US-09-605-573a-62	Sequence 62, Appl
	15	155	89.6 <td>35</td> <td>18</td> <td>US-09-433-428-64</td> <td>Sequence 64, Appl</td>	35	18	US-09-433-428-64	Sequence 64, Appl
	16	155	89.6 <td>35</td> <td>20</td> <td>US-09-605-573a-64</td> <td>Sequence 64, Appl</td>	35	20	US-09-605-573a-64	Sequence 64, Appl
	17	134	77.5 <td>23</td> <td>18</td> <td>US-09-433-428-61</td> <td>Sequence 61, Appl</td>	23	18	US-09-433-428-61	Sequence 61, Appl
	18	134	77.5 <td>23</td> <td>20</td> <td>US-09-605-573a-61</td> <td>Sequence 61, Appl</td>	23	20	US-09-605-573a-61	Sequence 61, Appl
	19	133	76.9 <td>23</td> <td>18</td> <td>US-09-433-428-59</td> <td>Sequence 59, Appl</td>	23	18	US-09-433-428-59	Sequence 59, Appl
	20	133	76.9 <td>23</td> <td>20</td> <td>US-09-605-573a-59</td> <td>Sequence 59, Appl</td>	23	20	US-09-605-573a-59	Sequence 59, Appl
	21	132	76.3 <td>23</td> <td>18</td> <td>US-09-433-428-60</td> <td>Sequence 60, Appl</td>	23	18	US-09-433-428-60	Sequence 60, Appl
	22	132	76.3 <td>23</td> <td>20</td> <td>US-09-605-573a-60</td> <td>Sequence 60, Appl</td>	23	20	US-09-605-573a-60	Sequence 60, Appl
	23	131	75.7 <td>33</td> <td>18</td> <td>US-09-433-428-30</td> <td>Sequence 30, Appl</td>	33	18	US-09-433-428-30	Sequence 30, Appl
	24	131	75.7 <td>33</td> <td>20</td> <td>US-09-605-573a-30</td> <td>Sequence 30, Appl</td>	33	20	US-09-605-573a-30	Sequence 30, Appl
	25	130	75.1 <td>32</td> <td>15</td> <td>US-09-147-362-11</td> <td>Sequence 11, Appl</td>	32	15	US-09-147-362-11	Sequence 11, Appl
	26	130	75.1 <td>32</td> <td>18</td> <td>US-09-147-362-11</td> <td>Sequence 11, Appl</td>	32	18	US-09-147-362-11	Sequence 11, Appl
	27	130	75.1 <td>33</td> <td>18</td> <td>US-09-433-428-23</td> <td>Sequence 23, Appl</td>	33	18	US-09-433-428-23	Sequence 23, Appl
	28	130	75.1 <td>33</td> <td>20</td> <td>US-09-605-573a-23</td> <td>Sequence 23, Appl</td>	33	20	US-09-605-573a-23	Sequence 23, Appl
	29	130	75.1 <td>113</td> <td>18</td> <td>US-09-462-917a-18</td> <td>Sequence 18, Appl</td>	113	18	US-09-462-917a-18	Sequence 18, Appl
	30	129	74.6 <td>33</td> <td>18</td> <td>US-09-433-428-25</td> <td>Sequence 25, Appl</td>	33	18	US-09-433-428-25	Sequence 25, Appl
	31	129	74.6 <td>33</td> <td>20</td> <td>US-09-605-573a-25</td> <td>Sequence 25, Appl</td>	33	20	US-09-605-573a-25	Sequence 25, Appl
	32	128	74.0 <td>33</td> <td>18</td> <td>US-09-433-428-2</td> <td>Sequence 2, Appl</td>	33	18	US-09-433-428-2	Sequence 2, Appl
	33	128	74.0 <td>33</td> <td>20</td> <td>US-09-605-573a-2</td> <td>Sequence 2, Appl</td>	33	20	US-09-605-573a-2	Sequence 2, Appl
	34	128	74.0 <td>33</td> <td>18</td> <td>US-09-433-428-10</td> <td>Sequence 10, Appl</td>	33	18	US-09-433-428-10	Sequence 10, Appl
	35	128	74.0 <td>33</td> <td>20</td> <td>US-09-605-573a-10</td> <td>Sequence 10, Appl</td>	33	20	US-09-605-573a-10	Sequence 10, Appl
	36	128	74.0 <td>33</td> <td>18</td> <td>US-09-433-428-12</td> <td>Sequence 12, Appl</td>	33	18	US-09-433-428-12	Sequence 12, Appl
	37	128	74.0 <td>33</td> <td>20</td> <td>US-09-605-573a-12</td> <td>Sequence 12, Appl</td>	33	20	US-09-605-573a-12	Sequence 12, Appl
	38	128	74.0 <td>33</td> <td>18</td> <td>US-09-433-428-13</td> <td>Sequence 13, Appl</td>	33	18	US-09-433-428-13	Sequence 13, Appl
	39	128	74.0 <td>33</td> <td>20</td> <td>US-09-605-573a-9</td> <td>Sequence 9, Appl</td>	33	20	US-09-605-573a-9	Sequence 9, Appl
	40	128	74.0 <td>33</td> <td>20</td> <td>US-09-605-573a-10</td> <td>Sequence 10, Appl</td>	33	20	US-09-605-573a-10	Sequence 10, Appl
	41	128	74.0 <td>33</td> <td>20</td> <td>US-09-605-573a-12</td> <td>Sequence 12, Appl</td>	33	20	US-09-605-573a-12	Sequence 12, Appl
	42	128	74.0 <td>33</td> <td>15</td> <td>US-09-147-362-21</td> <td>Sequence 21, Appl</td>	33	15	US-09-147-362-21	Sequence 21, Appl
	43	128	74.0 <td>35</td> <td>15</td> <td>US-09-147-362-21</td> <td>Sequence 21, Appl</td>	35	15	US-09-147-362-21	Sequence 21, Appl
	44	128	74.0 <td>35</td> <td>22</td> <td>US-09-886-149-62</td> <td>Sequence 62, Appl</td>	35	22	US-09-886-149-62	Sequence 62, Appl
	45	128	74.0 <td>35</td> <td>22</td> <td>US-09-886-150-62</td> <td>Sequence 62, Appl</td>	35	22	US-09-886-150-62	Sequence 62, Appl

ALIGNMENTS

RESULT 1

US-09-433-428-69

Sequence 69, Application US/09433428

GENERAL INFORMATION:

APPLICANT: Zheng, Jian

TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O

FILE REFERENCE: CDS-207

CURRENT APPLICATION NUMBER: US/09/433,428

CURRENT FILING DATE: 1999-11-04

NUMBER OF SEQ ID NOS: 69

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 69

LENGTH: 30

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: HIV Consensus

US-09-433-428-69

Query Match 100.0%; Score 173; DB 18; Length 30;
Best Local Similarity 100.0%; Pred. No. 7e-17;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GRETLMODODRLNSWCKGRICITSARWH 30

1 GRETLMODODRLNSWCKGRICITSARWH 30

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RESULT      6
US-09-605-573A-67
: Sequence 67, Application US/09605573A
: GENERAL INFORMATION:
: APPLICANT: De Leys, Robert J.
: APPLICANT: Zheng, Jian
: TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
: FILE REFERENCE: CDS-222
: CURRENT APPLICATION NUMBER: US/09/605,573A
: CURRENT FILING DATE: 2000-06-28
: NUMBER OF SEQ ID NOS: 70
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 67
: LENGTH: 149
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: HIV Consensus
: OTHER INFORMATION: Sequence

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; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 57
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:HIV Consensus
US-09-433-428-57
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Query Match          90.8%; Score 157; DB 18; Length 439;
Best Local Similarity 96.4%; Pred. No. 1.8e-13;
Matches 27; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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OY 3 ETLMOOQRLNSWGCKGRITCYTSARWH 30
|||||:|||||:|||||:|||||:|||||
DB 240 ETLMOOQRLNSWGCKGRITCYTSARWH 267
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RESULT 12
US-09-605-573A-57
; Sequence 57, Application US/09605573A
; GENERAL INFORMATION:
; APPLICANT: De Leys, Robert J.
; APPLICANT: Zheng, Jian
; TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
; FILE REFERENCE: CDS-222
; CURRENT APPLICATION NUMBER: US/09/605,573A
; CURRENT FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 57
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:HIV Consensus
US-09-605-573A-57
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Query Match          90.8%; Score 157; DB 20; Length 439;
Best Local Similarity 96.4%; Pred. No. 1.8e-13;
Matches 27; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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```
OY 3 ETLMOOQRLNSWGCKGRITCYTSARWH 30
|||||:|||||:|||||:|||||:|||||
DB 240 ETLMOOQRLNSWGCKGRITCYTSARWH 267
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US-09-433-428-62
; Sequence 62, Application US/09433428
; GENERAL INFORMATION:
; APPLICANT: De Leys, Robert J.
; APPLICANT: Zheng, Jian
; TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
; FILE REFERENCE: CDS-207
; CURRENT APPLICATION NUMBER: US/09/433,428
; CURRENT FILING DATE: 1999-11-04
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 62
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:HIV Consensus
US-09-433-428-62
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Query Match          89.6%; Score 155; DB 18; Length 28;
Best Local Similarity 96.4%; Pred. No. 2.4e-14;
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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OY 3 ETLMOOQRLNSWGCKGRITCYTSARWH 30
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DB 1 ETLMOOQRLNSWGCKGRITCYTSARWH 28
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; Sequence 62, Application US/09605573A
; GENERAL INFORMATION:
; APPLICANT: De Leys, Robert J.
; APPLICANT: Zheng, Jian
; TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
; FILE REFERENCE: CDS-222
; CURRENT APPLICATION NUMBER: US/09/605,573A
; CURRENT FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 62
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Xaa is any amino acid
; LOCATION: 6
; OTHER INFORMATION: Description of Artificial Sequence:HIV Consensus
US-09-605-573A-62
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Query Match          89.6%; Score 155; DB 20; Length 28;
Best Local Similarity 96.4%; Pred. No. 2.4e-14;
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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OY 3 ETLMOOQRLNSWGCKGRITCYTSARWH 30
|||||:|||||:|||||:|||||
DB 1 ETLMOOQRLNSWGCKGRITCYTSARWH 28
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RESULT 15
US-09-433-428-64
; Sequence 64, Application US/09433428
; GENERAL INFORMATION:
; APPLICANT: De Leys, Robert J.
; APPLICANT: Zheng, Jian
; TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
; FILE REFERENCE: CDS-207
; CURRENT APPLICATION NUMBER: US/09/433,428
; CURRENT FILING DATE: 1999-11-04
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 64
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:HIV Consensus
US-09-433-428-64
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Query Match          89.6%; Score 155; DB 18; Length 35;
Best Local Similarity 96.4%; Pred. No. 3e-14;
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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OY 3 ETLMOOQRLNSWGCKGRITCYTSARWH 30
|||||:|||||:|||||:|||||
DB 8 ETLMOOQRLNSWGCKGRITCYTSARWH 35
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Fri Jun 21 10:39:05 2002

us-09-605-573a-69.rapm

Page 5

Search completed: June 20, 2002, 15:34:04
Job time: 212 sec

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SEQ ID NO 23
LENGTH: 849
TYPE: PRT
ORGANISM: Human immunodeficiency virus
US-09-899-575-23

Query Match 49.1%; Score 85; DB 5; Length 849;
Best Local Similarity 46.4%; Pred. No. 0.00043;
Matches 13; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 3 ETLMDDOORLNSWGCKGRITCYTSARWH 30
Db 577 ERYLKDQDLGIMGCGSKLICITTAVPWN 604

RESULT 3
US-09-913-159A-2
Sequence 2, Application US/09913159A
GENERAL INFORMATION:
APPLICANT: Strathmann AG & Co.
TITLE OF INVENTION: Virus-Vaccine
FILE REFERENCE: P057760
CURRENT APPLICATION NUMBER: US/09/913,159A
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: 199 07 485.2
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 854
TYPE: PRT
ORGANISM: Human immunodeficiency virus
FEATURE:
OTHER INFORMATION: Envelope Polypeptide
US-09-913-159A-2

Query Match 49.1%; Score 85; DB 5; Length 854;
Best Local Similarity 46.4%; Pred. No. 0.00043;
Matches 13; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 3 ETLMDDOORLNSWGCKGRITCYTSARWH 30
Db 582 ERYLKDQDLGIMGCGSKLICITTAVPWN 609

RESULT 4
US-09-899-575-24
Sequence 24, Application US/09899575
GENERAL INFORMATION:
APPLICANT: Zur Megele, Jan
APPLICANT: Barnett, Susan W.
APPLICANT: Egnelbrecht, Susan
APPLICANT: van Rensburg, Estrella Janse
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C
FILE REFERENCE: P01631.102
CURRENT APPLICATION NUMBER: US/09/899,575
PRIOR FILING DATE: 2001-07-05
PRIOR APPLICATION NUMBER: 09/475,704
NUMBER OF SEQ ID NOS: 135
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 24
LENGTH: 855
TYPE: PRT
ORGANISM: Human immunodeficiency virus
US-09-899-575-24

Query Match 49.1%; Score 85; DB 5; Length 855;
Best Local Similarity 46.4%; Pred. No. 0.00043;

Matches 13; Conservative 6; Mismatches 9; Indels 0; Gaps 0;
QY 3 ETLMDDOORLNSWGCKGRITCYTSARWH 30
Db 576 ERYLKDQDLGIMGCGSKLICITTAVPWN 603

RESULT 5
US-10-130-157-363
Sequence 363, Application US/10130157
GENERAL INFORMATION:
APPLICANT: GENPART GmbH
TITLE OF INVENTION: The Genome of the HIV-1 Inter-Subtype (C/B') and Use Thereof
FILE REFERENCE: WAG-001 PCT
CURRENT APPLICATION NUMBER: US/10/130,157
PRIOR FILING DATE: 2002-05-14
PRIOR APPLICATION NUMBER: DE 19955089.1
PRIOR FILING DATE: 1999-11-16
NUMBER OF SEQ ID NOS: 379
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 363
LENGTH: 867
TYPE: PRT
ORGANISM: Human immunodeficiency virus
US-10-130-157-363

Query Match 49.1%; Score 85; DB 6; Length 867;
Best Local Similarity 46.4%; Pred. No. 0.00044;
Matches 13; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 3 ETLMDDOORLNSWGCKGRITCYTSARWH 30
Db 588 ERYLKDQDLGIMGCGSKLICITTAVPWN 615

RESULT 6
US-08-776-188B-8
Sequence 8, Application US/08776188B
GENERAL INFORMATION:
APPLICANT: Weinhuess, Ursula-Henrike
APPLICANT: Kruse-Muller, Cornelia
APPLICANT: Hoss, Eva
APPLICANT: Faatz, Elke
APPLICANT: Ofenloch-Hahne, Beatus
APPLICANT: Seidel, Christoph
APPLICANT: Wiedmann, Michael
TITLE OF INVENTION: DETERMINATION OF A SPECIFIC IMMUNOGLOBULIN USING MULTIPLE ANTI
FILE REFERENCE: 100564-07003
CURRENT APPLICATION NUMBER: US/08/776,188B
PRIOR FILING DATE: 2002-04-15
PRIOR APPLICATION NUMBER: PCT/EP95/02919
PRIOR FILING DATE: 1995-07-24
PRIOR APPLICATION NUMBER: P 44 30 972.4
PRIOR FILING DATE: 1994-08-31
PRIOR APPLICATION NUMBER: P 44 26 276.0
PRIOR FILING DATE: 1994-07-25
NUMBER OF SEQ ID NOS: 76
SOFTWARE: PatentIn version 3.1
SEQ ID NO 8
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Epitope region of HIV I or
US-08-776-188B-8

Query Match 41.6%; Score 72; DB 4; Length 15;
Best Local Similarity 66.7%; Pred. No. 0.00052;
Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 12 LNSMCKGRIICYTS 26
1:|||||:|||||
DB 1 LSLMCKGKLVCYTS 15

RESULT 7
US-08-776-188B-19
Sequence 19, Application US/08776188B
GENERAL INFORMATION:
APPLICANT: Weinhuess, Ursula-Henrike
APPLICANT: Kruse-Muller, Cornelia
APPLICANT: Hoss, Eva
APPLICANT: Faatz, Elke
APPLICANT: Offenloch-Hahnle, Beatus
APPLICANT: Seidel, Christoph
APPLICANT: Wiedmann, Michael
TITLE OF INVENTION: DETERMINATION OF A SPECIFIC IMMUNOGLOBULIN USING MULTIPLE ANTIGEN
FILE REFERENCE: 100564-07003
CURRENT APPLICATION NUMBER: US/08/776,188B
CURRENT FILING DATE: 2002-04-15
PRIOR APPLICATION NUMBER: PCT/EP95/02919
PRIOR FILING DATE: 1995-07-24
PRIOR APPLICATION NUMBER: P 44 30 972.4
PRIOR FILING DATE: 1994-08-31
PRIOR APPLICATION NUMBER: P 44 26 276.0
PRIOR FILING DATE: 1994-07-25
NUMBER OF SEQ ID NOS: 76
SOFTWARE: PatentIn version 3.1
SEQ ID NO 19
LENGTH: 19
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE: OTHER INFORMATION: Description of Artificial Sequence: SH-activated linear peptide 9
NAME/KEY: misc_feature
LOCATION: (2)..(2)
OTHER INFORMATION: Xaa at position 2 is Beta-alanine
FEATURE:
NAME/KEY: misc_feature
LOCATION: (3)..(3)
OTHER INFORMATION: Xaa at position 3 is Epsilon-aminocaproic acid
FEATURE:
NAME/KEY: misc_feature
LOCATION: (4)..(4)
OTHER INFORMATION: Xaa at position 4 is Beta-alanine
US-08-776-188B-19

Query Match 41.6%; Score 72; DB 4; Length 19;
Best Local Similarity 66.7%; Pred. No. 0.00066;
Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 12 LNSMCKGRIICYTS 26
1:|||||:|||||
DB 5 LSLMCKGKLVCYTS 19

RESULT 8
US-08-776-188B-36
Sequence 36, Application US/08776188B
GENERAL INFORMATION:
APPLICANT: Weinhuess, Ursula-Henrike
APPLICANT: Kruse-Muller, Cornelia
APPLICANT: Hoss, Eva
APPLICANT: Faatz, Elke
APPLICANT: Offenloch-Hahnle, Beatus
APPLICANT: Seidel, Christoph
APPLICANT: Wiedmann, Michael
TITLE OF INVENTION: DETERMINATION OF A SPECIFIC IMMUNOGLOBULIN USING MULTIPLE ANTIGEN
FILE REFERENCE: 100564-07003
CURRENT APPLICATION NUMBER: US/08/776,188B
CURRENT FILING DATE: 2002-04-15

PRIOR APPLICATION NUMBER: PCT/EP95/02919
PRIOR FILING DATE: 1995-07-24
PRIOR APPLICATION NUMBER: P 44 30 972.4
PRIOR FILING DATE: 1994-08-31
PRIOR APPLICATION NUMBER: P 44 26 276.0
PRIOR FILING DATE: 1994-07-25
NUMBER OF SEQ ID NOS: 76
SOFTWARE: PatentIn version 3.1
SEQ ID NO 36
LENGTH: 19
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Digoxigenin-labelled linear
OTHER INFORMATION: gp41/2
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(1)
OTHER INFORMATION: Xaa at position 1 is digoxigenin-3-cme
FEATURE:
NAME/KEY: misc_feature
LOCATION: (2)..(2)
OTHER INFORMATION: Xaa at position 2 is Beta-alanine
FEATURE:
NAME/KEY: misc_feature
LOCATION: (3)..(3)
OTHER INFORMATION: Xaa at position 3 is Epsilon-aminocaproic acid
FEATURE:
NAME/KEY: misc_feature
LOCATION: (4)..(4)
OTHER INFORMATION: Xaa at position 4 is Beta-alanine
US-08-776-188B-36

Query Match 41.6%; Score 72; DB 4; Length 19;
Best Local Similarity 66.7%; Pred. No. 0.00066;
Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 12 LNSMCKGRIICYTS 26
1:|||||:|||||
DB 5 LSLMCKGKLVCYTS 19

RESULT 9
US-09-576-824A-20
Sequence 20, Application US/09576824A
GENERAL INFORMATION:
APPLICANT: De Leys, Robert
TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES CORRESPONDING
TITLE OF INVENTION: TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR USE IN
TITLE OF INVENTION: A PROCESS FOR DETERMINATION OF ANTIBODIES OF
TITLE OF INVENTION: BIOTINYLATED PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORT
TITLE OF INVENTION: EPITOPES, A PROCESS FOR PREPARING THEM AND COMPOSITIONS
TITLE OF INVENTION: CONTAINING THEM
FILE REFERENCE: 2752-11
CURRENT APPLICATION NUMBER: US/09/576,824A
CURRENT FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 08/723,425
PRIOR FILING DATE: 1996-09-30
PRIOR APPLICATION NUMBER: 09/146,028
PRIOR FILING DATE: 1993-11-22
PRIOR APPLICATION NUMBER: PCT/EP93/00517
PRIOR FILING DATE: 1993-03-08
PRIOR APPLICATION NUMBER: EP 92400598.6
PRIOR FILING DATE: 1992-03-06
NUMBER OF SEQ ID NOS: 600
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 20
LENGTH: 22
TYPE: PRT
ORGANISM: Human Immunodeficiency virus
FEATURE:
NAME/KEY: VARIANT

LOCATION: (1)
OTHER INFORMATION: modified site
NAME/KEY: VARIANT
LOCATION: (22)
OTHER INFORMATION: modified site
US-09-576-824A-20

Query Match 41.6%; Score 72; DB 5; Length 22;
Best Local Similarity 66.7%; Pred. No. 0.00077;
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 6 MODORLNSGCKGRITC 23
DB 4 LQDQRLNSGCAFRVCHTVPM 21

RESULT 10
US-08-776-188B-10
Sequence 10 Application US/08776188B
GENERAL INFORMATION:
APPLICANT: Weinues, Ursula-Henrike
APPLICANT: Kruse-Muller, Cornelia
APPLICANT: Hoss, Eva
APPLICANT: Faatz, Elke
APPLICANT: Offenloch-Hahnle, Beatus
APPLICANT: Seidel, Christoph
APPLICANT: Wiedmann, Michael
TITLE OF INVENTION: DETERMINATION OF A SPECIFIC IMMUNOGLOBULIN USING MULTIPLE ANTIGEN
FILE REFERENCE: 100564-07003
CURRENT APPLICATION NUMBER: US/08/776,188B
CURRENT FILING DATE: 2002-04-15
PRIOR APPLICATION NUMBER: PCT/EP95/02919
PRIOR FILING DATE: 1995-07-24
PRIOR APPLICATION NUMBER: P 44 30 972.4
PRIOR FILING DATE: 1994-08-31
PRIOR APPLICATION NUMBER: P 44 26 276.0
PRIOR FILING DATE: 1994-07-25
NUMBER OF SEQ ID NOS: 76
SOFTWARE: Patentin version 3.1
SEQ ID NO 10
LENGTH: 27
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Epitope region of HIV I or HI
US-08-776-188B-10

Query Match 41.6%; Score 72; DB 4; Length 27;
Best Local Similarity 52.4%; Pred. No. 0.00094;
Matches 11; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 9 QORLNSGCKGRITCYTSARW 29
DB 1 QAOILNSGCAFRVCHTVPM 21

RESULT 11
US-08-776-188B-54
Sequence 54 Application US/08776188B
GENERAL INFORMATION:
APPLICANT: Weinues, Ursula-Henrike
APPLICANT: Kruse-Muller, Cornelia
APPLICANT: Hoss, Eva
APPLICANT: Faatz, Elke
APPLICANT: Offenloch-Hahnle, Beatus
APPLICANT: Seidel, Christoph
APPLICANT: Wiedmann, Michael
TITLE OF INVENTION: DETERMINATION OF A SPECIFIC IMMUNOGLOBULIN USING MULTIPLE ANTIGEN
FILE REFERENCE: 100564-07003
CURRENT APPLICATION NUMBER: US/08/776,188B

CURRENT FILING DATE: 2002-04-15
PRIOR APPLICATION NUMBER: PCT/EP95/02919
PRIOR FILING DATE: 1995-07-24
PRIOR APPLICATION NUMBER: P 44 30 972.4
PRIOR FILING DATE: 1994-08-31
PRIOR APPLICATION NUMBER: P 44 26 276.0
PRIOR FILING DATE: 1994-07-25
NUMBER OF SEQ ID NOS: 76
SOFTWARE: Patentin version 3.1
SEQ ID NO 54
LENGTH: 31
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Ruthenylated linear peptid
NAME/KEY: misc_feature
LOCATION: (1)..(1)
OTHER INFORMATION: Xaa at position 1 is BPRu
US-08-776-188B-54

Query Match 41.6%; Score 72; DB 4; Length 31;
Best Local Similarity 52.4%; Pred. No. 0.0011;
Matches 11; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 9 QORLNSGCKGRITCYTSARW 29
DB 5 QAOILNSGCAFRVCHTVPM 25

RESULT 12
US-09-359-975-14
Sequence 14 Application US/09359975
GENERAL INFORMATION:
APPLICANT: Weiner, David B.
APPLICANT: Williams, William V.
Mang, Bin
TITLE OF INVENTION: Compositions and Methods for Delivery of
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESS: Woodcock Washburn Kurtz Mackiewicz & Norris
STREET: One Liberty Place 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 mb-MD/JAF
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/359,975
FILING DATE: 23-JUL-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/979,385B
FILING DATE: 26-NOV-1997
APPLICATION NUMBER: US 08/495,684
FILING DATE: 28-SEP-1995
APPLICATION NUMBER: PCT/US94/00899
FILING DATE: 26-JAN-1994
APPLICATION NUMBER: 08/125,012
FILING DATE: 21-SEP-1993
APPLICATION NUMBER: 08/124,962
FILING DATE: 21-SEP-1993
APPLICATION NUMBER: 08/093,235
FILING DATE: 15-JUL-1993
APPLICATION NUMBER: 08/029,336
FILING DATE: 11-MAR-1993
APPLICATION NUMBER: 08/008,342

```

; FILING DATE: 26-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: UPAP-0253
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3429
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-359-975-14

Query Match          40.5%; Score 70; DB 5; Length 26;
Best Local Similarity 52.4%; Pred. No. 0.0018;
Matches 11; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY      3  ETLMDQRLNSGCKGRITC 23
DB      6  ERYIKDQDLGIMGCSGKLC 26

RESULT 13
US-08-776-188B-5
; Sequence 5, Application US/08776188B
; GENERAL INFORMATION:
; APPLICANT: Weinhuess, Ursula-Henrike
; APPLICANT: Kruse-Muller, Cornelia
; APPLICANT: Hoss, Eva
; APPLICANT: Paatz, Elke
; APPLICANT: Offenloch-Hahnle, Beatus
; APPLICANT: Seidel, Christoph
; APPLICANT: Wiedmann, Michael
; TITLE OF INVENTION: DETERMINATION OF A SPECIFIC IMMUNOGLOBULIN USING MULTIPLE ANTIGEN
; FILE REFERENCE: 100564-07003
; CURRENT APPLICATION NUMBER: US/08/776,188B
; CURRENT FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: PCT/EP95/02919
; PRIOR FILING DATE: 1995-07-24
; PRIOR APPLICATION NUMBER: P 44 30 972.4
; PRIOR FILING DATE: 1994-08-31
; PRIOR APPLICATION NUMBER: P 44 26 276.0
; PRIOR FILING DATE: 1994-07-25
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Epitope region of HIV 1 or HI
; OTHER INFORMATION: HIV subtype O
US-08-776-188B-5

Query Match          37.6%; Score 65; DB 4; Length 23;
Best Local Similarity 47.4%; Pred. No. 0.008;
Matches 9; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY      12 LNSMGCKGRITCYTSARWH 30
DB      1  LGIMGCSGKLCITTAVPWN 19

RESULT 14
US-09-576-824A-6
; Sequence 6, Application US/09576824A
; GENERAL INFORMATION:
; APPLICANT: De Leys, Robert
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES CORRESPONDING
; TITLE OF INVENTION: TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR USE IN
; TITLE OF INVENTION: A PROCESS FOR DETERMINATION OF ANTIBODIES OF
; TITLE OF INVENTION: BIOTINYLATED PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORT
; TITLE OF INVENTION: EPITOPES, A PROCESS FOR PREPARING THEM AND COMPOSITIONS
; FILE REFERENCE: 2752-11
; CURRENT APPLICATION NUMBER: US/09/576,824A
; CURRENT FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 08/723,425
; PRIOR FILING DATE: 1996-09-30
; PRIOR APPLICATION NUMBER: 09/146,028
; PRIOR FILING DATE: 1993-11-22
; PRIOR APPLICATION NUMBER: PCT/EP93/00517
; PRIOR FILING DATE: 1993-03-08
; PRIOR APPLICATION NUMBER: EP 92400598.6
; PRIOR FILING DATE: 1992-03-06
; NUMBER OF SEQ ID NOS: 600
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)
; OTHER INFORMATION: modified site
; NAME/KEY: VARIANT
; LOCATION: (24)
; OTHER INFORMATION: modified site
US-09-576-824A-6

Query Match          32.1%; Score 55.5; DB 5; Length 24;
Best Local Similarity 47.8%; Pred. No. 0.19;
Matches 11; Conservative 4; Mismatches 8; Indels 1; Gaps 1;

QY      8  DQRLNSGCKGRITCYTSARWH 30
DB      2  DQDLGIMGCSGKRLT-TVPPWN 23

RESULT 15
US-08-776-188B-30
; Sequence 30, Application US/08776188B
; GENERAL INFORMATION:
; APPLICANT: Weinhuess, Ursula-Henrike
; APPLICANT: Kruse-Muller, Cornelia
; APPLICANT: Hoss, Eva
; APPLICANT: Paatz, Elke
; APPLICANT: Offenloch-Hahnle, Beatus
; APPLICANT: Seidel, Christoph
; APPLICANT: Wiedmann, Michael
; TITLE OF INVENTION: DETERMINATION OF A SPECIFIC IMMUNOGLOBULIN USING MULTIPLE ANTI
; FILE REFERENCE: 100564-07003
; CURRENT APPLICATION NUMBER: US/08/776,188B
; CURRENT FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: PCT/EP95/02919
; PRIOR FILING DATE: 1995-07-24
; PRIOR APPLICATION NUMBER: P 44 30 972.4
; PRIOR FILING DATE: 1994-08-31
; PRIOR APPLICATION NUMBER: P 44 26 276.0
; PRIOR FILING DATE: 1994-07-25
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Digoxigenin-labelled linea
; OTHER INFORMATION: gp41/2
```

```

; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: Xaa at position 1 is digoxigenin-3-cme
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2)..(2)
; OTHER INFORMATION: Xaa at position 2 is Beta-alanine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (3)..(3)
; OTHER INFORMATION: Xaa at position 3 is Epsilon-aminocaproic acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4)..(4)
; OTHER INFORMATION: Xaa at position 4 is Beta-alanine
US-08-776-188B-30

```

```

Query Match      31.8%; Score 55; DB 4; Length 20;
Best Local Similarity 53.3%; Pred. No. 0.19;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 12 LNSWCKGRIICYTS 26
   | | | | : | | | :
Db 5 LGIMCGSGKLICTTA 19

```

Search completed: June 20, 2002, 15:34:57
 Job time: 205 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 20, 2002, 15:28:32 ; Search time 14.82 Seconds
(without alignments)
194.513 Million cell updates/sec

Title: US-09-605-573a-69
173
Perfect score: 1 GRETLMDDOORLNSMGCKGRITCYTSARWH 30
Sequence:

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR.71:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	118	68.2	104	2 S52930	GP41 ENV protein -
2	116	67.1	863	2 A53034	gag polyprotein -
3	114	65.9	877	2 SA9197	envelope protein p
4	93	53.8	854	1 VCLJST	env polyprotein pr
5	92	53.2	858	1 VCLJG2	env polyprotein pr
6	89	51.4	864	1 VCLJG4	envelope protein g
7	88	50.9	357	2 S21990	envelope protein g
8	88	50.9	358	2 S22002	envelope protein g
9	87	50.3	358	2 S23000	envelope protein g
10	87	50.3	358	2 S70417	envelope protein g
11	87	50.3	859	1 VCLJST	env polyprotein pr
12	86	49.7	151	2 S30448	env protein - huma
13	86	49.7	151	2 S30453	env protein - huma
14	86	49.7	151	2 S30452	env protein - huma
15	86	49.7	151	2 S30450	env protein - huma
16	86	49.7	151	2 S30451	env protein - huma
17	86	49.7	151	2 S30457	env protein - huma
18	85	49.1	151	2 S30456	env protein - huma
19	85	49.1	151	2 S30455	env protein - huma
20	85	49.1	151	2 S30454	env protein - huma
21	85	49.1	357	2 S22006	envelope protein g
22	85	49.1	357	2 S21994	envelope protein g
23	85	49.1	357	2 S22004	envelope protein g
24	85	49.1	357	2 S21996	envelope protein g
25	85	49.1	357	2 S21992	envelope protein g
26	85	49.1	358	2 S21998	envelope protein p
27	85	49.1	358	2 C41621	env polyprotein p
28	85	49.1	445	2 A41621	env polyprotein M
29	85	49.1	445	2 A41621	env polyprotein M

30	85	49.1	454	2 B41621	env polyprotein D
31	85	49.1	843	1 H44001	env polyprotein pr
32	85	49.1	852	1 VCLJBR	env polyprotein pr
33	85	49.1	852	2 T12016	envelope glycoprote
34	85	49.1	853	2 S54384	envelope polyprote
35	85	49.1	854	2 S13288	env protein - huma
36	85	49.1	855	1 VCLJAZ	env polyprotein pr
37	85	49.1	855	1 VCLJZR	env polyprotein pr
38	85	49.1	856	1 VCLJH3	env polyprotein pr
39	85	49.1	856	1 VCLJLV	env polyprotein pr
40	85	49.1	856	1 VCLJ3W	env polyprotein pr
41	85	49.1	859	1 VCLJMN	env polyprotein pr
42	85	49.1	861	1 VCLJLV	env polyprotein pr
43	85	49.1	861	1 VCLJSC	env polyprotein pr
44	85	49.1	868	1 VCLJH4	env polyprotein -
45	84	48.6	151	2 S30458	env protein - huma

ALIGNMENTS

RESULT 1
S52930
GP41 ENV protein - human immunodeficiency virus type 1 (fragment)
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 06-Jun-1995 #sequence_revision 21-Jul-1995 #text_change 26-Aug-1999
C:Accession: S52930
R:Cohen, J.H.M.; Gueard, D.; Philibert, F.; Chamaret, S.; Tabary, T.; Montagnier, L.;
submitted to the EMBL Data Library, January 1995
A:Description: A novel HIV-1 O strain illustrates the diversity of the O group.
A:Reference number: S52929
A:Accession: S52930
A:Status: preliminary
A:Molecule type: genomic RNA
A:Residues: 1-104 <COH>
A:Cross-references: EMBL:X84328; NID:G695526; PIDN:CA59066.1; PID:G695527
C:Superfamily: type E retrovirus env polyprotein

Query Match 68.2% Score 118; DB 2; Length 104;
Best Local Similarity 67.9% Pred. No. 1.2e-09;
Matches 19; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 3 ETLMDDOORLNSMGCKGRITCYTSARWH 30
||||| 11 11111:||||| 1:
DB 37 ETLMDDOORLNSMGCKGRITCYTSARWH 64

RESULT 2
gag polyprotein - human immunodeficiency virus type 1 (strain Ant70)
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 07-May-1999
C:Accession: A53034
R:Yanden Haesevelde, M.; Decourt, J.L.; De Leys, R.J.; Vandeborght, B.; van der Groe
J. Virol. 68: 1586-1596, 1994
A:Title: Genomic cloning and complete sequence analysis of a highly divergent African
A:Reference number: A53034; MUID:94149849
A:Accession: A53034
A:Status: preliminary
A:Molecule type: genomic RNA
A:Residues: 1-863 <VAN>
A:Cross-references: GB:I02587
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: polyprotein

Query Match 67.1% Score 116; DB 2; Length 863;
Best Local Similarity 60.7% Pred. No. 1.7e-08;
Matches 17; Conservative 8; Mismatches 3; Indels 0; Gaps 0;
QY 3 ETLMDDOORLNSMGCKGRITCYTSARWH 30
||||| 11 11111:||||| 1:

Db 586 ETLNODQRLNSWGCGRICVTSARW 613

RESULT 3

549197

envelope protein precursor - human immunodeficiency virus type 1 (fragment)

C:Species: human immunodeficiency virus type 1, HIV-1

C>Date: 19-Mar-1997 #sequence_revision 24-Jul-1997 #text_change 26-Aug-1999

C:Accession: S49197

R:Chaneau, P.; Borman, A.M.; Quillent, C.; Guetard, D.; Chamaret, S.; Cohen, J.; Remy, submitted to the EMBL Data Library, July 1994

A:Description: Isolation and envelope sequence of a highly divergent HIV-1 isolate: defi

A:Reference number: S49197

A:Accession: S49197

A:Molecule type: DNA

A:Residues: 1-877 <CH>

A:Cross-references: EMBL:X80020; NID:9510516; PIDN:CAA56323.1; PID:9510517

A:Experimental source: isolate VAV

C:Superfamily: type E retrovirus env polyprotein

C:Keywords: glycoprotein; capsid protein; coat protein; transmembrane protein

F:1-30/Domain: signal sequence #status predicted <SIG>

F:31-537/Product: coat protein gp120 #status predicted <CP1>

F:538-877/Product: coat protein gp41 #status predicted <CP2>

F:878-916/Domain: transmembrane #status predicted <TMN>

F:59,88,139,148,159,184,188,198,230,235,242,263,270,277,292,302,333,345,357,367,396,404,

Query Match

Best Local Similarity 65.9%; Score 114; DB 2; Length 877;

Matches 18; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 3 ETLNODQRLNSWGCGRICVTSARW 30

Db 599 ETLNODQRLNSWGCGRICVTSARW 626

RESULT 4

VCLJST

env polyprotein precursor - simian immunodeficiency virus SIVcpz

N:Alternate names: coat polyprotein

C:Species: simian immunodeficiency virus SIVcpz

A:Note: host Pan troglodytes (chimpanzee)

C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999

C:Accession: S09990

R:Huet, T.; Chénier, R.; Meyerhans, A.; Roelants, G.; Waln-Hobson, S.

Nature 345, 356-359, 1990

A:Title: Genetic organization of a chimpanzee lentivirus related to HIV-1.

A:Reference number: S09983; MUID:90259077

A:Accession: S09990

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-854 <HUE>

A:Cross-references: EMBL:X52154; NID:958866; PIDN:CAA36407.1; PID:958874

C:Genetics:

A:Gene: env

C:Superfamily: type E retrovirus env polyprotein

C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp

F:1-30/Domain: signal sequence #status predicted <SIG>

F:31-500/Product: coat protein gp120 #status predicted <CP1>

F:501-854/Product: coat protein gp41 #status predicted <CP2>

F:855-916/Domain: transmembrane #status predicted <TM1>

F:675-693/Domain: transmembrane #status predicted <TM2>

F:805-821/Domain: transmembrane #status predicted <TM3>

F:134,140,143,158,186,195,239,260,267,274,299,331,336,351,356,384,392,426,432,446,45

Query Match

Best Local Similarity 53.8%; Score 93; DB 1; Length 854;

Matches 14; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 3 ETLNODQRLNSWGCGRICVTSARW 30

Db 574 ERYLDDQRLNSWGCGRICVTSARW 601

RESULT 5

VCLJG2

env polyprotein precursor - human immunodeficiency virus type 2 (isolate ROD)

N:Alternate names: coat polyprotein

C:Species: human immunodeficiency virus type 2, HIV-2

C>Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 16-Jul-1999

C:Accession: C26262

R:Gardner, M.; Emerman, M.; Sonigo, P.; Clavel, F.; Montagnier, L.; Alizon, M.

Nature 336, 662-669, 1987

A:Title: Genome organization and transactivation of the human immunodeficiency virus

A:Reference number: A26262; MUID:8713056

A:Contents: proviral DNA

A:Accession: C26262

A:Molecule type: DNA

A:Residues: 1-858 <GU>

A:Cross-references: GB:M15390; NID:g1332361; PIDN:AAB00770.1; PID:g325749

C:Genetics:

A:Gene: env

C:Superfamily: type E retrovirus env polyprotein

C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp

F:1-17/Domain: signal sequence #status predicted <SIG>

F:18-858/Product: env polyprotein #status predicted <MAT>

F:859-916/Product: exterior membrane glycoprotein #status predicted <EXT>

F:502-858/Product: transmembrane glycoprotein #status predicted <TMN>

F:34,67,76,119,120,151,166,179,192,193,196,206,238,241,248,272,278,289,300,367,371,40

Query Match

Best Local Similarity 53.2%; Score 92; DB 1; Length 858;

Matches 15; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 3 ERYLDDQRLNSWGCGRICVTSARW 29

Db 583 ERYLDDQRLNSWGCGRICVTSARW 609

RESULT 6

VCLJG4

env polyprotein - simian immunodeficiency virus (African green monkey isolate)

C:Species: simian immunodeficiency virus, SIV

C>Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 24-Oct-1997

C:Accession: G30045

R:Fukushima, M.; Miura, T.; Hasegawa, A.; Morikawa, S.; Tsujimoto, H.; Miki, K.; Kitam

Nature 333, 457-461, 1988

A:Title: Sequence of simian immunodeficiency virus from African green monkey, a new m

A:Reference number: A30045; MUID:88232906

A:Accession: G30045

A:Molecule type: DNA

A:Residues: 1-864 <FUK>

A:Cross-references: EMBL:X07805

C:Genetics:

A:Gene: env

C:Superfamily: type E retrovirus env polyprotein

C:Keywords: AIDS; capsid protein; coat protein; immunodeficiency; polyprotein; trans

Query Match

Best Local Similarity 51.4%; Score 89; DB 1; Length 864;

Matches 13; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 3 ERYLDDQRLNSWGCGRICVTSARW 29

Db 608 ERYLDDQRLNSWGCGRICVTSARW 634

RESULT 7

S21990

envelope protein gp120/gp41 - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1

A:Variety: isolate 20

C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
C:Accession: S21990; S70423
R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
submitted to the EMBL Data Library, July 1991
A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined
A:Reference number: S21990
A:Accession: S21990
A:Molecule type: DNA
A:Residues: 1-357 <STE1>
A:Cross-references: EMBL:X61357; NID:g60175; PID:CAA43626.1; PID:g60176
R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid
A:Reference number: S70417; MUID:92144209
A:Accession: S70423
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-332, 'X', 334-357 <STE2>
A:Cross-references: EMBL:X61357; NID:g60175; PID:CAA43626.1; PID:g60176
C:Superfamily: type E retrovirus env polypotein

Query Match 50.9%; Score 88; DB 2; Length 357;
Best Local Similarity 50.0%; Pred. No. 7.2e-05;
Matches 14; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 3 ETLMDQORLNSWCKGRITCYTSARWH 30
| : : | | | | | | | | | | : : |
DB 85 ERYLKDQDLGLTIGWCGSRILCTTAVPMW 113

RESULT 8
S22002
envelope protein gp120/gp41 - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
A:Variety: isolate 3L
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
C:Accession: S22002; S70418
R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
submitted to the EMBL Data Library, July 1991
A:Title: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined
A:Reference number: S21990
A:Accession: S22002
A:Molecule type: DNA
A:Residues: 1-358 <STE1>
A:Cross-references: EMBL:X61352; NID:g60186; PID:CAA43616.1; PID:g60187
R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid
A:Reference number: S70417; MUID:92144209
A:Accession: S70418
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-333, 'X', 335-358 <STE2>
A:Cross-references: EMBL:X61352; NID:g60186
C:Superfamily: type E retrovirus env polypotein

Query Match 50.9%; Score 88; DB 2; Length 358;
Best Local Similarity 50.0%; Pred. No. 7.2e-05;
Matches 14; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 3 ETLMDQORLNSWCKGRITCYTSARWH 30
| : : | | | | | | | | | | : : |
DB 86 ERYLKDQDLGLTIGWCGSRILCTTAVPMW 113

RESULT 9
S22000
envelope protein gp120/gp41 - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 12-Apr-1995
C:Accession: S22000

R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
submitted to the EMBL Data Library, July 1991
A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined
A:Reference number: S21990
A:Accession: S22000
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-358 <STE>
A:Cross-references: EMBL:X61351
C:Superfamily: type E retrovirus env polypotein

Query Match 50.3%; Score 87; DB 2; Length 358;
Best Local Similarity 50.0%; Pred. No. 0.0001;
Matches 14; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 3 ETLMDQORLNSWCKGRITCYTSARWH 30
| : : | | | | | | | | | | : : |
DB 86 ERYLKDQDLGLTIGWCGSRILCTTAVPMW 113

RESULT 10
S70417
envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 3B) (fragment)
C:Species: human immunodeficiency virus type 1, HIV-1
A:Variety: patient 3B
C>Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 26-Aug-1999
C:Accession: S70417
R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid
A:Reference number: S70417; MUID:92144209
A:Accession: S70417
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-358 <STE>
A:Cross-references: EMBL:X61351; NID:g60184; PID:CAA43614.1; PID:g60185
C:Superfamily: type E retrovirus env polypotein

Query Match 50.3%; Score 87; DB 2; Length 358;
Best Local Similarity 50.0%; Pred. No. 0.0001;
Matches 14; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 3 ETLMDQORLNSWCKGRITCYTSARWH 30
| : : | | | | | | | | | | : : |
DB 86 ERYLKDQDLGLTIGWCGSRILCTTAVPMW 113

RESULT 11
VCLJST
env polypotein precursor - human immunodeficiency virus type 2 (isolate, ST)
N:Alternate names: coat polypotein
N:Contains: surface glycoprotein gp120; transmembrane glycoprotein gp41
C:Species: human immunodeficiency virus type 2, HIV-2
A>Note: host Homo sapiens (man)
C>Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Sep-1994
C:Accession: H33943
R:Kumar, P.; Hul, H.; Kappes, J.C.; Haggarty, B.S.; Hoxie, J.A.; Arya, S.K.; Shaw, G.
J. Virol. 64, 890-901, 1990
A:Title: Molecular characterization of an attenuated human immunodeficiency virus type 2
A:Reference number: A33943; MUID:90112662
A:Accession: H33943
A:Molecule type: genomic RNA
A:Residues: 1-859 <KUM>
A:Cross-references: EMBL:M86924
C:Genetics: env
C:Superfamily: type E retrovirus env polypotein
C:Keywords: coat protein; glycoprotein; polypotein; transmembrane protein
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-859/Product: env polypotein #status predicted <ENV>
F:20-501/Product: surface glycoprotein gp120 #status predicted <SGG>

Query Match 49.7%; Score 86; DB 2; Length 151;
 Best Local Similarity 48.1%; Pred. No. 6.2e-05;
 Matches 13; Conservative 6; Mismatches 8; Indels 0; Gaps 0;
 QY 3 ETLMDQDQRLNSWGCGRITCTTSARW 29
 |::||:||||| |:|:|
 DB 28 EKYLNDAQRLNSWGCAPROVCHTTEW 54

Search completed: June 20, 2002, 15:32:12
 Job time: 220 sec

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Query Match	Best Local Similarity	Score 93;	DB 1;	Length 854;
Matches 14;	Conservative 5;	Mismatches 9;	Indels 0;	Gaps 0;
Oy	3	ETIMODQORLNSMGCKGRICYSARWH 30		
Db	574	ERYLDQDQIILGMGSGKAVCTTTPMN 601		
RESULT	2			
ENV_HV2KR				
ID	ENV_HV2KR	STANDARD;	PRT;	857 AA.
AC	074126;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	Envelope glycoprotein gp160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].			
GN	ENV.			
OS	Human immunodeficiency virus type 2 (isolate KR) (HIV-2).			
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.			
OX	NCBI_TaxID=73484;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Kraus G.K., Talbot R., Leavitt M., Luzznick L., Schmidt A., Babel P., Bartz C., Morton W., Wong-Staal F., Looney D.J.;			
RL	Submitted (Apr-1995) to the EMBL/Genbank/DBJ databases.			
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CC	-----			
DR	EMBL; U22047; AAA64582.1; -			
DR	InterPro; IPR000328; Env_GP41.			
DR	InterPro; IPR000777; GP120.			
DR	Pfam; PF00516; GP120.1.			
KW	Pfam; PF00517; GP41.1.			
FT	AIDS; Coat protein; Glycoprotein; Transmembrane; Signal.			
FT	SIGNAL	1	19	POTENTIAL.
FT	CHAIN	20	503	EXTERIOR MEMBRANE GLYCOPROTEIN.
FT	CHAIN	504	857	TRANSMEMBRANE GLYCOPROTEIN.
FT	CARBOHYD	36	36	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	69	69	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	78	78	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	113	113	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	121	121	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	134	134	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	142	142	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	159	159	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	186	186	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	198	198	N-LINKED (GLCNAC. . .) (POTENTIAL).

FT	CARBOHYD	230	230	N-LINKED (GLCNAC. . .)	(POTENTIAL).		
FT	CARBOHYD	233	233	N-LINKED (GLCNAC. . .)	(POTENTIAL).		
FT	CARBOHYD	264	264	N-LINKED (GLCNAC. . .)	(POTENTIAL).		
FT	CARBOHYD	270	270	N-LINKED (GLCNAC. . .)	(POTENTIAL).		
FT	CARBOHYD	281	281	N-LINKED (GLCNAC. . .)	(POTENTIAL).		
FT	CARBOHYD	292	292	N-LINKED (GLCNAC. . .)	(POTENTIAL).		
FT	CARBOHYD	302	302	N-LINKED (GLCNAC. . .)	(POTENTIAL).		
FT	CARBOHYD	358	358	N-LINKED (GLCNAC. . .)	(POTENTIAL).		
FT	CARBOHYD	364	364	N-LINKED (GLCNAC. . .)	(POTENTIAL).		
FT	CARBOHYD	391	391	N-LINKED (GLCNAC. . .)	(POTENTIAL).		
FT	CARBOHYD	440	440	N-LINKED (GLCNAC. . .)	(POTENTIAL).		
FT	CARBOHYD	455	455	N-LINKED (GLCNAC. . .)	(POTENTIAL).		
FT	CARBOHYD	603	603	N-LINKED (GLCNAC. . .)	(POTENTIAL).		
FT	CARBOHYD	612	612	N-LINKED (GLCNAC. . .)	(POTENTIAL).		
FT	CARBOHYD	628	628	N-LINKED (GLCNAC. . .)	(POTENTIAL).		
SO	SEQUENCE	857 AA;	98689 MW;	P881C6755B5746DF	CNC64;		
Query Match		53.8%;	Score 93;	DB 1;	Length 857;		
Best Local Similarity		55.6%;	Pred. No. 2.7e-06;				
Matches 15;		Conservative 4;	No.matches 8;	Indels 0;	Gaps 0;		
Oy	3 ETLMDDOORLNSWGCKGRLLICTSARW 29						
... :							
Db	575 EKYLRDQARLNSWGCAFRQVCITYLW 601						
RESULT 3							
ENV_HV2RO	STANDARD;	PRT;	858 AA.				
ID	ENV_HV2RO						
AC	P04577;						
DT	13-AUG-1987 (Rel. 05, Created)						
DT	13-AUG-1987 (Rel. 05, Last sequence update)						
DT	16-OCT-2001 (Rel. 40, Last annotation update)						
DE	Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].						
DE	ENV.						
GN	Human immunodeficiency virus type 2 (isolate ROD) (HIV-2).						
OS	Viruses; Retrovird viruses; Retroviridae; Lentivirus.						
OC	NCBI_TaxID=11720;						
OX	[1]						
RN	SEQUENCE FROM N.A.						
RP	MEDLINE=87173056; PubMed=3031510;						
RX	Guyader M., Emerman M., Sonigo P., Clavel F., Montagnier L.,						
RA	Alizon M.;						
RT	"Genome organization and transactivation of the human						
RT	immunodeficiency virus type 2.";						
RL	Nature 326:662-669(1987).						
CC	-----						
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CC	-----						
CC	EMBL; M15390; AAB00770.1; -;						
DR	EMBL; X05291; CA28914.1; -;						
DR	PIR; C26262; VCL02.						
DR	HIV; M15390; ENV52ROD.						
DR	InterPro; IPR000328; ENV_GP41.						
DR	InterPro; IPR000777; GP120.						
DR	Pfam; PF00516; GP120.1.						
DR	Pfam; PF00517; GP41.1.						
KW	AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;						
KW	Signal.						
FT	SIGNAL	1	17				
FT	CHAIN	18					

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FT CARBOHYD 119 119 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 120 120 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 166 166 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 179 179 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 192 192 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 193 193 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 196 196 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 206 206 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 248 248 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 272 272 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 278 278 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 300 300 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 310 310 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 367 367 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 371 371 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 410 410 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 447 447 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 466 466 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 620 620 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 636 636 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 312 312 T -> I (IN REF 1; AAB00770).
SQ SEQUENCE 838 AA; 98824 MW; C7266AF1F5C5B9A7 CRC64;

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Query Match 53.2%; Score 92; DB 1; Length 858;
Best Local Similarity 55.6%; Pred. No. 3.9e-06;
Matches 15; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

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OY 3 ETLMDQORLNSWCGKGRILCYTSARW 29
DB 583 EKYLDQARLNSWCGKAFRCVCHTTPW 609

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RESULT 4
ENV_SIVAT STANDARD: PRT; 865 AA.
ID ENV_SIVAT
AC P05886;
DT 01-NOV-1988 (Rel. 09; Last sequence update)
DT 16-OCT-2001 (Rel. 40; Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Simian immunodeficiency virus (TYO-1 isolate) (SIV-AGM).
OC Viruses; Retroviral viruses; Retroviridae; Lentiviruses.
OX NCBI_TaxID=11731;
RN [1]
RX MEDLINE=88232906; PubMed=3374586;
RA Fukusawa M., Miura T., Hasegawa A., Morikawa S., Tsujimoto H.,
MIKI K., Kitamura T., Hayami M.;
RT "Sequence of simian immunodeficiency virus from African green monkey,
a new member of the HIV/SIV group.";
RL Nature 333:457-461(1988).
CC -1- MISCELLANEOUS: THIS IS AN AFRICAN GREEN MONKEY ISOLATE.
CC -----
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CC -----
CC DR EMBL; X07805; CAA30663.2;
CC PIR; G30045; VCLG4.

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DR HIV; X07805; ENV$AGMTY.
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
DR Aids; Coat protein; Glycoprotein; Transmembrane;
Signal.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 536 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 537 865 TRANSMEMBRANE GLYCOPROTEIN.
FT SITE 770 770 IN-FRAME TERMINATION CODON.
FT CARBOHYD 35 35 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 68 68 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 117 117 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 150 150 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 210 210 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 252 252 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 255 255 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 266 266 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 282 282 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 294 294 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 306 306 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 316 316 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 373 373 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 414 414 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 451 451 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 488 488 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 491 491 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 645 645 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 661 661 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 865 AA; 99024 MW; 6CEFD0F09001D6D95 CRC64;

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Query Match 51.4%; Score 89; DB 1; Length 865;
Best Local Similarity 48.1%; Pred. No. 1.1e-05;
Matches 13; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

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OY 3 ETLMDQORLNSWCGKGRILCYTSARW 29
DB 608 EKYLDQARLNSWCGKAMKOVCHTTEW 634

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RESULT 5
ENV_SIVAT STANDARD: PRT; 854 AA.
ID ENV_SIVAT
AC 002837;
DT 01-JUL-1993 (Rel. 26; Last sequence update)
DT 16-OCT-2001 (Rel. 40; Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Simian immunodeficiency virus (isolate AGM / clone GRI-1) (SIV-AGM).
OC Viruses; Retroviral viruses; Retroviridae; Lentiviruses.
OX NCBI_TaxID=31684;
RN [1]
RX MEDLINE=91220680; PubMed=2024476;
RA Fomsgaard A., Hirsch V.M., Allan J.S., Johnson P.R.;
RT "A highly divergent proviral DNA clone of SIV from a distinct species
of African green monkey.";
RL Virology 182:397-402(1991).
CC -1- MISCELLANEOUS: THIS IS AN AFRICAN GREEN MONKEY ISOLATE.
CC -----
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CC CC

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CC -----

DR EMBL; M66437; AAA91928.1; -

DR EMBL; M58410; AAA47591.1; -

DR InterPro; IPR000328; Env_Gp41.

DR InterPro; IPR000777; GP120.

DR Pfam; PF00516; GP120; 1.

DR Pfam; PF00517; GP41; 1.

KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal.

FT SIGNAL 1 24 POTENTIAL.

FT CHAIN 25 522 EXTERIOR MEMBRANE GLYCOPROTEIN

FT CHAIN 523 854 TRANSMEMBRANE GLYCOPROTEIN

FT CARBOHYD 35 35 (POTENTIAL).

FT CARBOHYD 68 68 (POTENTIAL).

FT CARBOHYD 115 115 (POTENTIAL).

FT CARBOHYD 136 136 (POTENTIAL).

FT CARBOHYD 153 153 (POTENTIAL).

FT CARBOHYD 168 168 (POTENTIAL).

FT CARBOHYD 182 182 (POTENTIAL).

FT CARBOHYD 199 199 (POTENTIAL).

FT CARBOHYD 244 244 (POTENTIAL).

FT CARBOHYD 255 255 (POTENTIAL).

FT CARBOHYD 265 265 (POTENTIAL).

FT CARBOHYD 271 271 (POTENTIAL).

FT CARBOHYD 283 283 (POTENTIAL).

FT CARBOHYD 295 295 (POTENTIAL).

FT CARBOHYD 305 305 (POTENTIAL).

FT CARBOHYD 355 355 (POTENTIAL).

FT CARBOHYD 400 400 (POTENTIAL).

FT CARBOHYD 409 409 (POTENTIAL).

FT CARBOHYD 458 458 (POTENTIAL).

FT CARBOHYD 472 472 (POTENTIAL).

FT CARBOHYD 478 478 (POTENTIAL).

FT CARBOHYD 623 623 (POTENTIAL).

FT CARBOHYD 624 624 (POTENTIAL).

FT CARBOHYD 630 630 (POTENTIAL).

FT CARBOHYD 646 646 (POTENTIAL).

SO SEQUENCE 854 AA; 96855 MW; 5919CA6C9622912F CRC64;

Query Match 50.3%; Score 87; DB 1; Length 854;

Best Local Similarity 48.1%; Pred. No. 2.2e-05;

Matches 13; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

OY 3 ETLMDQOQLNSGCKGRITCYTSARW 29

Db 594 EKYLEDQARLNSGCAWQVCHTTPW 620

RESULT 6

ENV_HV2NZ STANDARD; PRT; 856 AA.

AC P05883;

DT 01-NOV-1988 (Rel. 09, Created)

DT 01-NOV-1988 (Rel. 09, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Envelope polyprotein GP160 precursor [contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].

GN ENV.

OS Human immunodeficiency virus type 2 (isolate NIH-2) (HIV-2).

OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.

OX NCBI_TaxID=11719;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=88320359; PubMed=3261862;

RA Zagury J.F., Francini G., Reitz M.S. Jr., Collalti E., Starcich B.R., Hall L., Fargnoli K., Jagodzinski L.L., Guo H.-G., Laure F., Ayra S.K., Josephs S.F., Zagury D., Wong-Staal F., Gallo R.C.;

RT Genetic variability between isolates of human immunodeficiency virus (HIV) type 2 is comparable to the variability among HIV type 1.

RL Proc. Natl. Acad. Sci. U.S.A. 85:5941-5945(1988).

CC -----

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CC -----

DR EMBL; J03654; AAB00761.1; -

DR HIV; J03654; ENV52NTH2.

DR InterPro; IPR000328; Env_Gp41.

DR InterPro; IPR000777; GP120.

DR Pfam; PF00516; GP120; 1.

DR Pfam; PF00517; GP41; 1.

KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal.

FT SIGNAL 1 20

FT CHAIN 21 492 EXTERIOR MEMBRANE GLYCOPROTEIN.

FT CHAIN 493 856 TRANSMEMBRANE GLYCOPROTEIN.

FT CARBOHYD 37 37 (POTENTIAL).

FT CARBOHYD 70 70 (POTENTIAL).

FT CARBOHYD 79 79 (POTENTIAL).

FT CARBOHYD 112 112 (POTENTIAL).

FT CARBOHYD 116 116 (POTENTIAL).

FT CARBOHYD 128 128 (POTENTIAL).

FT CARBOHYD 133 133 (POTENTIAL).

FT CARBOHYD 142 142 (POTENTIAL).

FT CARBOHYD 182 182 (POTENTIAL).

FT CARBOHYD 183 183 (POTENTIAL).

FT CARBOHYD 196 196 (POTENTIAL).

FT CARBOHYD 228 228 (POTENTIAL).

FT CARBOHYD 231 231 (POTENTIAL).

FT CARBOHYD 238 238 (POTENTIAL).

FT CARBOHYD 262 262 (POTENTIAL).

FT CARBOHYD 268 268 (POTENTIAL).

FT CARBOHYD 279 279 (POTENTIAL).

FT CARBOHYD 290 290 (POTENTIAL).

FT CARBOHYD 300 300 (POTENTIAL).

FT CARBOHYD 355 355 (POTENTIAL).

FT CARBOHYD 390 390 (POTENTIAL).

FT CARBOHYD 400 400 (POTENTIAL).

FT CARBOHYD 440 440 (POTENTIAL).

FT CARBOHYD 457 457 (POTENTIAL).

FT CARBOHYD 602 602 (POTENTIAL).

FT CARBOHYD 611 611 (POTENTIAL).

FT CARBOHYD 627 627 (POTENTIAL).

SO SEQUENCE 856 AA; 98665 MW; A938B0A7E2B881D6 CRC64;

Query Match 50.3%; Score 87; DB 1; Length 856;

Best Local Similarity 51.9%; Pred. No. 2.2e-05;

Matches 14; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

OY 3 ETLMDQOQLNSGCKGRITCYTSARW 29

Db 574 EKYLKDAQQLNSGCAFRVCHTSVPM 600

RESULT 7

ENV_HV2SB STANDARD; PRT; 846 AA.

AC P12449;

DT 01-OCT-1989 (Rel. 12, Created)

DT 01-OCT-1989 (Rel. 12, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Envelope polyprotein GP160 precursor [contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].

GN ENV.

OS Human immunodeficiency virus type 2 (isolate SBLISY) (HIV-2).

OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.

OX NCBI_TaxID=11718;

FT DISULFID 125 194 BY SIMILARITY.
 FT DISULFID 130 155 BY SIMILARITY.
 FT DISULFID 216 245 BY SIMILARITY.
 FT DISULFID 226 237 BY SIMILARITY.
 FT DISULFID 294 328 BY SIMILARITY.
 FT DISULFID 374 435 BY SIMILARITY.
 FT DISULFID 381 408 BY SIMILARITY.
 FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 154 154 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 232 232 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 239 239 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 260 260 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 274 274 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 299 299 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 329 329 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 336 336 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 352 352 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 382 382 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 388 388 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 438 438 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 454 454 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 602 602 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 628 628 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 847 AA: 96135 MW: 0A901317FD7PF2AB CRC64:

Query Match 49.1% Score 85: DB 1: Length 847;
 Best Local Similarity 46.4% Pred. No. 4.4e-05;
 Matches 13: Conservative 6; Mismatches 9; Indels 0; Gaps 0;

Oy 3 ETLMDQRLNSWGCKGRICYSARWH 30
 Db 575 ERYLDDQLGLWGSGKLCITTVPMW 602

RESULT 11
 ENV_HV1W2 STANDARD: PRT: 847 AA.
 AC P05880:
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV
 OS Human immunodeficiency virus type 1 (HIV-1) isolate (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentiviridae.
 OX NCBI_TaxID=11705;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86235450; PubMed=3012778;
 RA Hahn B.H., Shaw G.M., Taylor M.E., Redfield R.R., Markham P.D., Salathuddin S.Z., Wong-Staal F., Gallo R.C., Parks E.S., Parks W.P.;
 RT Genetic variation in HTLV-III/LAV over time in patients with AIDS or at risk for AIDS.
 RL Science 232:1548-1553(1986).
 CC -1- MISCELLANEOUS: ISOLATES WMJ1, WMJ2, AND WMJ3 WERE OBTAINED FROM BLOOD SAMPLES SEQUENTIALLY TAKEN FROM A TWO-YEAR OLD HAITIAN WHO WAS PERINATALLY INFECTED BY HER MOTHER.
 CC -----
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 CC -----

DR EMBL: M12507; AAB12990.1; -
 DR HIV: M12507; ENVSMWJ2.
 DR InterPro: IPR000328; ENV_GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120.1.
 DR Pfam: PF00517; GP41.1.
 KW Aids; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal.

FT SIGNAL 1 29
 FT CHAIN 30 501
 FT CHAIN 502 847
 FT DISULFID 53 73 TRANSMEMBRANE GLYCOPROTEIN.
 FT DISULFID 118 202 BY SIMILARITY.
 FT DISULFID 125 193 BY SIMILARITY.
 FT DISULFID 130 152 BY SIMILARITY.
 FT DISULFID 215 244 BY SIMILARITY.
 FT DISULFID 225 236 BY SIMILARITY.
 FT DISULFID 293 326 BY SIMILARITY.
 FT DISULFID 372 435 BY SIMILARITY.
 FT CARBOHYD 379 408 BY SIMILARITY.
 FT CARBOHYD 134 134 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 155 155 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 184 184 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 194 194 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 231 231 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 259 259 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 273 273 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 286 286 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 292 292 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 327 327 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 334 334 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 350 350 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 380 380 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 438 438 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 450 450 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 602 602 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 628 628 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 847 AA: 96466 MW: CDIE33D73AASBCAE CRC64:

Query Match 49.1% Score 85: DB 1: Length 847;
 Best Local Similarity 46.4% Pred. No. 4.4e-05;
 Matches 13: Conservative 6; Mismatches 9; Indels 0; Gaps 0;

Oy 3 ETLMDQRLNSWGCKGRICYSARWH 30
 Db 575 ERYLDDQLGLWGSGKLCITTVPMW 602

RESULT 12
 ENV_HV1B8 STANDARD: PRT: 851 AA.
 AC P04582:
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV

GN	HUMAN.
OS	Human immunodeficiency virus type 1 (BH8 isolate) (HIV-1).
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX	NCBI_TaxID=11684;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=8511123; PubMed=2578615;
RA	Ratner L., Haseltine W., Patarca R., Livak K.J., Starcich B.R.,
RA	Josephs S.F., Dorian E.R., Rafalski J.A., Whitehorn E.A.,
RA	Bammeister K., Ivanoff L., Pettenay S.R. Jr., Pearson M.L.,
RA	Lautenberger J.A., Papas T.S., Ghraieb J., Chang N.T., Gallo R.C.,
RT	Wong-Staal F.;
RL	"Complete nucleotide sequence of the AIDS virus, HTLV-III.";
CC	Nature 313:277-284(1985).
CC-	-----
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CC	or send an email to license@isb-sib.ch).
CC	-----
DR	EMBL, K02011; AAAA461.1; .
DR	HIV, K02011; ENV5B8.
DR	GlycoSuiteDB, P04582; .
DR	InterPro, IPR000328; Env-GP1.
DR	Interpro, IPR000777; GP120.
DR	Pfam, PF00516; GP120; 1.
DR	Pfam, PF00517; GP41; 1.
KW	AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
KW	Signal.
FT	SIGNAL.
FT	CHAIN
FT	31 506
FT	507 851
FT	DISULFID
FT	54 74
FT	DISULFID
FT	119 205
FT	DISULFID
FT	126 196
FT	DISULFID
FT	131 157
FT	DISULFID
FT	218 247
FT	DISULFID
FT	228 239
FT	DISULFID
FT	296 331
FT	DISULFID
FT	378 440
FT	DISULFID
FT	385 413
FT	CARBOHYD
FT	88 88
FT	CARBOHYD
FT	136 136
FT	CARBOHYD
FT	141 141
FT	CARBOHYD
FT	156 156
FT	CARBOHYD
FT	160 160
FT	CARBOHYD
FT	186 186
FT	CARBOHYD
FT	197 197
FT	CARBOHYD
FT	220 220
FT	CARBOHYD
FT	234 234
FT	CARBOHYD
FT	241 241
FT	CARBOHYD
FT	262 262
FT	CARBOHYD
FT	276 276
FT	CARBOHYD
FT	295 295
FT	CARBOHYD
FT	301 301
FT	CARBOHYD
FT	332 332
FT	CARBOHYD
FT	339 339
FT	CARBOHYD
FT	356 356
FT	CARBOHYD
FT	386 386
FT	CARBOHYD
FT	392 392
FT	CARBOHYD
FT	401 401
FT	CARBOHYD
FT	443 443
FT	CARBOHYD
FT	458 458
FT	CARBOHYD
FT	606 606
FT	CARBOHYD
FT	611 611
FT	CARBOHYD
FT	620 620
FT	CARBOHYD
FT	632 632
FT	CARBOHYD
FT	669 669
FT	CARBOHYD
FT	745 745
FT	CARBOHYD
FT	811 811

SQ	SEQUENCE	851 AA;	96644 MW;	D16A3C90857785F1 CRC64;
	Query Match	49.1%;	Score 85;	DB 1; Length 851;
	Best Local Similarity	46.4%;	Pred. No.	4.4e-05;
	Matches 13;	Conservative	6; Mismatches	9; Indels 0; Gaps 0;
OY	3 ETLMODQRLSNMGCKGRITCYTSARWH 30 :: : :			
Db	579 ERYLKDQQLLIGWCGSKLICTTAVPMW 606			
	RESULT 13			
ID	ENV_HV1BN	STANDARD;	PRT;	852 AA.
AC	P12488;			
DT	01-OCT-1989 (Rel. 12, Created)			
DT	01-OCT-1989 (Rel. 12, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP11)].			
CN	ENV.			
OS	Human immunodeficiency virus type 1 (IBR isolate) (HIV-1).			
OC	Vituses; Retroid viruses; Retroviridae; Lentivirus.			
OX	MCLT_faxid-11693; [1]			
RN	SEQUENCE FROM N.A.			
RP	MEDLINE=89085613; PubMed=2789516;			
RX	Anand R., Thayer R., Srinivasan A., Nayyar S., Gardner M., Luciw P., Dandekar S.;			
RA	"Biological and molecular characterization of human immunodeficiency virus (HIV-1BR) from the brain of a patient with progressive dementia.";			
RT	-I- MISCELLANEOUS: THIS VIRUS IS CYTOPATHICALLY ACTIVE AND WAS HARVESTED FROM THE BRAIN TISSUE OF A NEUROLOGICAL AIDS PATIENT.			
RL	Virology 168:79-89(1989).			
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CC	EMBL; M21098: AAA44221.1; .			
DR	PIR; A31667; VCLJBR.			
DR	HIV; M21098; ENVSBRVA.			
DR	InterPro; IPR000328; Env_GP41.			
DR	InterPro; IPR000777; GP120.			
DR	pfam; PF00516; GP120; 1. pfam; PF00517; GP41; 1.			
KM	AIDS; Coat protein; Polypotein; Glycopoltein; Transmembrane; Signal.			
FT	SIGNAL	1	30	
FT	CHAIN	31	507	EXTERIOR MEMBRANE GLYCOPROTEIN.
FT	CHAIN	508	852	TRANSMEMBRANE GLYCOPROTEIN.
FT	DISULFD	54	74	BY SIMILARITY.
FT	DISULFD	119	205	BY SIMILARITY.
FT	DISULFD	126	196	BY SIMILARITY.
FT	DISULFD	131	155	BY SIMILARITY.
FT	DISULFD	218	247	BY SIMILARITY.
FT	DISULFD	228	239	BY SIMILARITY.
FT	DISULFD	296	330	BY SIMILARITY.
FT	DISULFD	376	439	BY SIMILARITY.
FT	DISULFD	383	412	BY SIMILARITY.
FT	CAROXYD	49	49	N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CAROXYD	88	88	N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CAROXYD	135	135	N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CAROXYD	138	138	N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CAROXYD	154	154	N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CAROXYD	158	158	N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CAROXYD	197	197	N-LINKED (GLCNAC . .) (POTENTIAL).

FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 331 331 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 360 360 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 396 396 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 442 442 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 456 456 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 612 612 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 621 621 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 633 633 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 670 670 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 812 812 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 852 AA; 97203 MW; 2BB86345DEC915F CRC64;

Query Match 49.1%; Score 85; DB 1; Length 852;
 Best Local Similarity 46.4%; Pred. No. 4.4e-05;
 Matches 13; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 3 ETLMDQOORLNSMGCKRICYTSARWH 30
 Db 580 ERYLRDQQLGIMGCKSLCTTTVPWN 607

RESULT 14
 ID ENV_HV1S3 STANDARD: PRT: 852 AA.
 AC P19549;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (SF33 isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxId=11690;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90317906; PubMed=2370688;
 RA York-Higgins D., Cheng-Mayer C., Bauer D., Levy J.A., Dina D.;
 RT "Human immunodeficiency virus type 1 cellular host range, replication, and cytopathicity are linked to the envelope region of the viral genome.";
 RT J. Virol. 64:4016-4020(1990).
 RL -----
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 CC -----
 DR EMBL: M38427; AAA5067.1; -
 DR HIV: M38427; ENVSE83.
 DR InterPro: IPR000328; Env_GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 DR AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal.
 KW SIGNAL 1 31 BY SIMILARITY.

FT CHAIN 32 506
 FT CHAIN 507 852
 FT DISULFID 53 73
 FT DISULFID 118 206
 FT DISULFID 125 197
 FT DISULFID 130 156
 FT DISULFID 219 248
 FT DISULFID 229 240
 FT DISULFID 297 331
 FT DISULFID 377 439
 FT DISULFID 384 412
 FT CARBOHYD 87 87
 FT CARBOHYD 129 136
 FT CARBOHYD 136 136
 FT CARBOHYD 141 141
 FT CARBOHYD 142 142
 FT CARBOHYD 155 155
 FT CARBOHYD 159 159
 FT CARBOHYD 189 189
 FT CARBOHYD 198 198
 FT CARBOHYD 242 242
 FT CARBOHYD 263 263
 FT CARBOHYD 277 277
 FT CARBOHYD 290 290
 FT CARBOHYD 296 296
 FT CARBOHYD 332 332
 FT CARBOHYD 339 339
 FT CARBOHYD 355 355
 FT CARBOHYD 385 385
 FT CARBOHYD 391 391
 FT CARBOHYD 397 397
 FT CARBOHYD 401 401
 FT CARBOHYD 405 405
 FT CARBOHYD 442 442
 FT CARBOHYD 457 457
 FT CARBOHYD 607 607
 FT CARBOHYD 612 612
 FT CARBOHYD 621 621
 FT CARBOHYD 633 633
 FT CARBOHYD 812 812
 SQ SEQUENCE 852 AA; 96663 MW; E57BBF8D23C9910D CRC64;

Query Match 49.1%; Score 85; DB 1; Length 852;
 Best Local Similarity 46.4%; Pred. No. 4.4e-05;
 Matches 13; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 3 ETLMDQOORLNSMGCKRICYTSARWH 30
 Db 580 ERYLRDQQLGIMGCKSLCTTTVPWN 607

RESULT 15
 ID ENV_HV1NF STANDARD: PRT: 853 AA.
 AC P19551;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (MFA isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxId=11704;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90317877; PubMed=1695254;
 RA Stevenson M., Haggerty S., Lamont C., Mann A.M., Meter C., Wasilak A.;
 RT "Cloning and characterization of human immunodeficiency virus type 1 variants diminished in the ability to induce syncytium-independent cytolysis.";

RL J. Virol. 64:3792-3803(1990).

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CC or send an email to license@isb-sib.ch).

DR EMBL: M33943; AAA44850.1; -

DR HIV: M33943; ENVSMFA.

DR InterPro: IPR000328; Env.GP41.

DR InterPro: IPR000777; GP120.

DR Pfam: PF00516; GP120; 1.

DR Pfam: PF00517; GP41; 1.

KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;

KW Signal.

FT SIGNAL 1 30

FT CHAIN 31 509

FT CHARIN 510 853

FT DISULFID 54 74

FT DISULFID 119 203

FT DISULFID 126 194

FT DISULFID 131 157

FT DISULFID 216 245

FT DISULFID 226 237

FT DISULFID 294 329

FT DISULFID 376 443

FT DISULFID 383 416

FT DISULFID 88 88

FT CARBOHYD 136 136

FT CARBOHYD 141 141

FT CARBOHYD 156 156

FT CARBOHYD 160 160

FT CARBOHYD 186 186

FT CARBOHYD 195 195

FT CARBOHYD 232 232

FT CARBOHYD 239 239

FT CARBOHYD 260 260

FT CARBOHYD 274 274

FT CARBOHYD 287 287

FT CARBOHYD 293 293

FT CARBOHYD 299 299

FT CARBOHYD 330 330

FT CARBOHYD 354 354

FT CARBOHYD 384 384

FT CARBOHYD 390 390

FT CARBOHYD 395 395

FT CARBOHYD 404 404

FT CARBOHYD 446 446

FT CARBOHYD 461 461

FT CARBOHYD 609 609

FT CARBOHYD 614 614

FT CARBOHYD 623 623

FT CARBOHYD 635 635

FT CARBOHYD 672 672

FT CARBOHYD 748 748

FT CARBOHYD 814 814

SO SEQUENCE 853 AA; 96912 MW; 3377B93B6F22ABA CRC64;

Query Match 49.1%; Score 85; DB 1; Length 853;
Best Local Similarity 46.4%; Pred. No. 4.5e-05;
Matches 13; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

0Y 3 ETLMDQDQRLNSWGCGRITCYTSARWH 30
DB 582 ERYLKQDQLLGIMCGSKLICITTAVPWN 609

Search completed: June 20, 2002, 15:35:14

Job time: 202 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 20, 2002, 15:31:02 ; Search time 25.12 seconds
(without alignments)
206,602 Million cell updates/sec

Title: US-09-605-573A-69
Perfect score: 173
Sequence: 1 GRETLMODQRLNSWCKGRICYSARWH 30

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_19:*
1: SP_archaea:*
2: SP_bacteria:*
3: SP_fungi:*
4: SP_human:*
5: SP_invertebrate:*
6: SP_mammal:*
7: SP_mhc:*
8: SP_organelle:*
9: SP_phage:*
10: SP_plant:*
11: SP_rodent:*
12: SP_virus:*
13: SP_vertebrate:*
14: SP_unclassified:*
15: SP_virus:*
16: SP_bacteriap:*
17: SP_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	133	76.9	161	15	Q9IEB5 human immun
2	133	76.9	524	15	Q9IEB3 human immun
3	132	76.3	179	15	Q9IEB4 human immun
4	132	76.3	195	15	Q9IEC6 human immun
5	132	76.3	576	15	Q9IEF1 human immun
6	131	75.7	219	15	Q9IEC8 human immun
7	130	75.1	114	15	Q9IEC8 human immun
8	129	74.6	216	15	Q9IEC5 human immun
9	129	74.6	219	15	Q9IEB6 human immun
10	128	74.0	120	15	Q9IEB6 human immun
11	128	74.0	134	15	Q9IEB6 human immun
12	128	74.0	143	15	Q9IEB6 human immun
13	128	74.0	143	15	Q9IEB6 human immun
14	128	74.0	143	15	Q9IEB6 human immun
15	127	73.4	105	15	Q9IEB3 human immun
16	127	73.4	172	15	Q9IEB3 human immun

17	127	73.4	234	15	Q9IEC2 human immun
18	127	73.4	242	15	Q9IEB3 human immun
19	126	72.8	125	15	Q9IEB3 human immun
20	126	72.8	130	15	Q9IEB3 human immun
21	126	72.8	216	15	Q9IEB3 human immun
22	126	72.8	232	15	Q9IEB3 human immun
23	126	72.8	242	15	Q9IEB3 human immun
24	126	72.8	243	15	Q9IEB3 human immun
25	126	72.8	544	15	Q9IEB3 human immun
26	125	72.3	111	15	Q9IEB3 human immun
27	125	72.3	114	15	Q9IEB3 human immun
28	125	72.3	114	15	Q9IEB3 human immun
29	125	72.3	224	15	Q9IEB3 human immun
30	125	72.3	418	15	Q9IEB3 human immun
31	124	71.7	124	15	Q9IEB3 human immun
32	124	71.7	126	15	Q9IEB3 human immun
33	124	71.7	134	15	Q9IEB3 human immun
34	124	71.7	183	15	Q9IEB3 human immun
35	124	71.7	200	15	Q9IEB3 human immun
36	124	71.7	213	15	Q9IEB3 human immun
37	124	71.7	220	15	Q9IEB3 human immun
38	124	71.7	225	15	Q9IEB3 human immun
39	124	71.7	512	15	Q9IEB3 human immun
40	124	71.7	517	15	Q9IEB3 human immun
41	124	71.7	532	15	Q9IEB3 human immun
42	124	71.7	545	15	Q9IEB3 human immun
43	123	71.1	112	15	Q9IEB3 human immun
44	123	71.1	114	15	Q9IEB3 human immun
45	123	71.1	116	15	Q9IEB3 human immun

ALIGNMENTS

RESULT 1
ID Q9IEB5 PRELIMINARY; PRT; 161 AA.
AC Q9IEB5;
DT 01-OCT-2000 (TREMREL. 15, Created)
DT 01-OCT-2000 (TREMREL. 15, Last sequence update)
DT 01-DEC-2001 (TREMREL. 19, Last annotation update)
DE GP41 (FRAGMENT).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BCF57;
RA Roques P., Robertson D., Sandrine S., Christel D., Francois S.,
RT Philippe M.;
Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ236405; CAB96253.1; -
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 161
SQ SEQUENCE 161 AA; 19305 MW; 5E3AF197E1FDEB7C CRC64;

Query Match 76.9%; Score 133; DB 15; Length 161;
Best Local Similarity 78.6%; Pred. No. 7.5e-13;
Matches 22; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 3 ETLMDQRLNSWCKGRICYSARWH 30
DB 31 ETLMDQRLNSWCKGRICYSARWH 30
RESULT 2
Q9IEB3

AD	Q9TED3:	PRELIMINARY;	PTF:	524 AA.
AC	Q9TED3:			
DT	01-OCT-2000 (TREMBLrel. 15	Created)		
DT	01-OCT-2000 (TREMBLrel. 15	Last sequence update)		
DT	01-DEC-2001 (TREMBLrel. 19	Last annotation update)		
DE	ENV POLYPEPTIDE (FRAGMENT).			
GN	ENV.			
OS	Human immunodeficiency virus type 1.			
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.			
OX	NCBI_TaxID=11676;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BCF57;			
RA	Rouques P., Robertson D., Diamond F., Soussquiere S., Mauciere P.,			
RA	Hevy-1 group C phylogenetic analysis of C2-gp41 region."			
RT	Submitted (FEB-1999) to the EMBL/Genbank/DBJ databases.			
RL	Submitted (FEB-1999) to the EMBL/Genbank/DBJ databases.			
DR	EMBL; AJ133074; CAB96235.1; -			
DR	InterPro; IPR000328; Env-GP41.			
DR	InterPro; IPR000777; GP120.			
DR	Pfam; PF00516; GP120; 1.			
DR	Pfam; PF00517; GP41; 1.			
KW	AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.			
FT	NON_TER	1		
FT	NON_TER	524		
FT	NON_TER	524		
SQ	SEQUENCE	524 AA;	59109 MW;	C3D9F12207AEB41 CXC64;

Query Match	76.9%	Score 133;	DB 15;	Length 524;
Best Local Similarity	78.6%;	Pred. No. 2.7e-12;		
Matches 22;	Conservative	4;	Mismatches 2;	Indels 0;
				Gaps 0;

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QY      3  ETLMDDQRLNSWGCKGRIICYTSARWH 30
      |||:|:||||| ||||| ||||| :|:
Db      355 ETLLNQGRNLWGCKGRIICYTSVKN 38

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SEQ	SEQUENCE	179 AA	2125 MW	B060634FF1D4531B	CRC64
OS	Human immunodeficiency virus type 1.				
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.				
OX	NCBI_TaxID=11676;				
RP	- [1]				
RN	SEQUENCE FROM N.A.				
RC	STRAIN=BCF58;				
RA	Raques P., Robertson D., Sandrine S., Christel D., Francois S.,				
RA	Philippe M.;				
RT	Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates."				
RL	Submitted (JAN-1999) to the EMBL/Genbank/DBJ databases.				
DR	EMBL: AJ236406; CAB96254.1; "				
DR	InterPro: IPR000328; Env_GP41.				
DR	Pfam: PF00517; GP41; 1.				
KM	Transmembrane.				
FT	NON_TER	1	1		
FT	NON_TER	179	179		
SEQ	SEQUENCE	179 AA	2125 MW	B060634FF1D4531B	CRC64

Query Match	76.3%	Score 132	DB 15	Length 179
Best Local Similarity	78.6%	Pred No. 1.2e-12		
Matches 22	Conservative	5	Mismatches 1	Indels 0
				Gaps 0

```
QY      3 ETLMDOORLNSWGCKGRICYSARWH 30
        |||:||||: ||||| ||||| :|:
Db     34 ETLIQNOORLSWGCKGRICYTSAKWN 61
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SEQ	SEQUENCE	195 AA;	22964 MW;	2A6363CD0C66A65 CRC64;
RT	Non-TER	1	1	
FT	NON-TER	195	195	
SO	SEQUENCE	195 AA;	22964 MW;	2A6363CD0C66A65 CRC64;
OC	NCBI TaxID=11676;			
OS	Human immunodeficiency virus type 1.			
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.			
OX	NCBI TaxID=11676;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BCF06;			
RA	Rouques P., Robertson D., Sandrine S., Christel D., Francois S.,			
RA	Philippe M.;			
RT	Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates."			
RL	Submitted (Jan-1999) to the EMBL/Genbank/DBJ databases.			
DR	EMBL; AJ236393; CAB96242.1;			
DR	InterPro; IPR000328; Env-GP41.			
DR	Pfam; PF00517; GP41; 1.			
KW	Transmembrane.			
FT	NON-TER	1	1	
FT	NON-TER	195	195	
SO	SEQUENCE	195 AA;	22964 MW;	2A6363CD0C66A65 CRC64;

Query Match	76.38;	Score 132;	DB 15;	Length 195;
Best Local Similarity	78.68;	Pred. No. 1.3e-12;		
Matches	22;	Conservative	5;	Mismatches 1;
			Indels	0;
			Gaps	0

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QY      3 ETLMDOORLNSWGCKGRICYSARWH    30
        |||:||||:|||||||:|:|
Db     35 ETLIQNQRSLSWGCKGRICYSAKN    62
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Q9IEF1	5	PRELIMINARY;	PRT;	576 AA.
ID	Q9IEF1			
AC	Q9IEF1;			
DT	01-OCT-2000 (TREMBLrel. 15, Created)			
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)			
DE	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DT	ENV POLYPEPTIDE (FRAGMENT).			
GN	ENV.			
OS	Human immunodeficiency virus type 1.			
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.			
NCBI_TaxID=11676;				
RN	(1)			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BCF06;			
RA	Rouques P., Brun-Yvelin D., Diamond F., Sousgriere S., Mauciere P.,			
RT	Deplienne C., Robert-Valentin F., Dormont D.;			
RL	"HIV-1 group O phylogenetic analysis of C2-gp41 region."			
DR	Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AJ133056; CAB96217.1; "			
DR	InterPro; IPR000328; Env.Gp41.			
DR	InterPro; IPR000777; GP120.			
DR	Pfam; PF00516; GP120. 1.			
DR	Pfam; PF00517; GP41. 1.			
KW	AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.			
FT	NON_TER 1			
FT	NON_TER 576 576			
SEQUENCE	576 AA; 64977 MW; A21509P3C618195D CRC64;			

Query Match	76.3%;	Score 132;	DB 15;	Length 576;
Best Local Similarity	78.6%;	Pred. No. 4.3e-12;		
Matches 22;	Conservative	5;	Mismatches 1;	Indels 0;
				Gaps 0.

QY 3 ETLMQDQRLNSWGCKGRICYSARWH 30

Db 392 ETLIONOOLNSMGCKGRICVTSKWN 419

RESULT 6

09IEC8 PRELIMINARY; PRT; 219 AA.
 AC 09IEC8;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE GP41 (FRAGMENT).
 GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP STRAIN=BCF02;
 RC SEQUENCE FROM N.A.
 RA Roques P., Robertson D., Sandrine S., Christel D., Francois S.,
 RA Philippe M.;
 RT "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates."
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ236391; CAB96240.1; -
 DR InterPro: IPR000328; Env_GP41.
 DR Pfam: PF00517; GP41; 1.
 KW Transmembrane.
 FT NON_TER 1
 FT NON_TER 219
 SQ SEQUENCE 219 AA; 25363 MW; 85C2DC5B5F528907 CRC64;

Query Match

Best Local Similarity 75.7%; Score 131; DB 15; Length 219;
 Matches 21; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 3 ETLMOOQOLNSMGCKGRICVTSARWH 30
 |||:|||||:|||||:|||||:|||||:|
 Db 48 ETLIONOOLNSMGCKGRICVTSKWN 75

RESULT 7

040456 PRELIMINARY; PRT; 114 AA.
 AC 040456;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE ENVELOPE TRANSMEMBRANE GLYCOPROTEIN (FRAGMENT).
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GROUP O;
 RA Bilbillet-Ruche F., Ekasa E., Peeters M., Delaporte E.;
 RT "Molecular characterization of envelope transmembrane glycoprotein of
 RT 14 new human immunodeficiency virus type 1 group O strains from
 RT different African countries."
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL: Y09772; CAAT0911.1; -
 DR InterPro: IPR000328; Env_GP41.
 DR Pfam: PF00517; GP41; 1.
 KW Transmembrane.
 FT NON_TER 1
 FT NON_TER 114
 SQ SEQUENCE 114 AA; 13737 MW; 7907E77F5B51FA9D CRC64;

Query Match 75.1%; Score 130; DB 15; Length 114;
 Best Local Similarity 75.0%; Pred. No. 1.5e-12;
 Matches 21; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 3 ETLMOOQOLNSMGCKGRICVTSARWH 30
 |||:|||||:|||||:|||||:|||||:|
 Db 31 ETLMOOQOLNSMGCKGRICVTSKWN 58

RESULT 8

09IEC5 PRELIMINARY; PRT; 216 AA.
 AC 09IEC5;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE GP41 (FRAGMENT).
 GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP STRAIN=BCF07;
 RC SEQUENCE FROM N.A.
 RA Roques P., Robertson D., Sandrine S., Christel D., Francois S.,
 RA Philippe M.;
 RT "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates."
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ236394; CAB96243.1; -
 DR InterPro: IPR000328; Env_GP41.
 DR Pfam: PF00517; GP41; 1.
 KW Transmembrane.
 FT NON_TER 1
 FT NON_TER 216
 SQ SEQUENCE 216 AA; 25027 MW; 413AE9BF1B4FC9A CRC64;

Query Match

Best Local Similarity 74.6%; Score 129; DB 15; Length 216;
 Matches 20; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 3 ETLMOOQOLNSMGCKGRICVTSARWH 30
 |||:|||||:|||||:|||||:|||||:|
 Db 39 ETLIONOOLNSMGCKGRICVTSKWN 66

RESULT 9

09IEB6 PRELIMINARY; PRT; 219 AA.
 AC 09IEB6;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE GP41 (FRAGMENT).
 GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BCF14;
 RA Roques P., Robertson D., Sandrine S., Christel D., Francois S.,
 RA Philippe M.;
 RT "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates."
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ236404; CAB96252.1; -
 DR InterPro: IPR000328; Env_GP41.
 DR Pfam: PF00517; GP41; 1.
 KW Transmembrane.
 FT NON_TER 1
 FT NON_TER 219
 SQ SEQUENCE 219 AA; 25353 MW; F65829EB01520D91 CRC64;

Query Match 74.6%; Score 129; DB 15; Length 219;
 Best Local Similarity 71.4%; Pred. No. 4.4e-12;
 Matches 20; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy	3	ETLMODQRLNSWGCGRITCYTSARWH	30
		:: :: :	
Db	61	ETLIQMOQLNLNMGCGRIVCYTSARN	88

ID	Q79670	PRELIMINARY;	PRT;	876 AA
AC	Q79670;			

01-NOV-1996 (TREMBLrel. 01, Created)
01-NOV-1996 (TREMBLrel. 01, Last sequence update)
01-DEC-2001 (TREMBLrel. 19, Last annotation update)
ENVELOPE PROTEIN GP120/GP41.
ENV.

human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 NCBI_TaxID=11676;

SEQUENCE FROM N.A
MED.TNE-94140848

Gurtler L.G., Hauser P.H. Eboria

Zekeng L., Tsague J.M., Kaptue L., Von Brunn A., Knapp S.,

Cameroon."; *Journal of Virology* 68:1501-1502, 1994.

EMBL; L20571: AAA44864.1: -

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InterPro; IPR000328; Env_GP41
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InterPro; IPR000777; GP120
Pfam: PF00516; CB130.1
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Pfam; PF00517; GP41; 1

AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane sequence

SEQUENCE 8/6 AA; 99245 MW; A92F868E37522BAB CRC64;

Query Match	74.08;	Score 128;	DB 15;	Length 876;
Best Local Similarity	71.48;	Pred. No. 2.8e-11;		
Matches	20; Conservation			

conservative 0; Mismatches 2; Indels 0; Gaps 0;

596 ETLIQNGRLNLMGCKGKLI CYTSVKWN 623

RESULT 15

011939
11939
DATE: 11/19/39

PRELIMINARY; PRT; 105 AA.

01-JUL-1997 (TREMBLrel. 04, Created
01-JUL-1997)

01-JUL-1997 (TREMBLrel. 04, Last sequence update)

ENVELOPE GLYCOPROTEIN (FRAGMENT)

ENV.

Human Immunodeficiency Virus type 1
Viruses: Retroviridae

NCBI_TaxID=11676;

[1] SEQUENCE FROM

SEQUENCE FROM N.A
STRAIN=ABT063:

MEDLINE=97340911; Pubmed=9197385.

Brennan C.A., Hackett J. Jr., Zekeng L., Lund J.K., Vallart A.C., Nkomo D.E.

Devarre S.G.; Gutfeller L., Kaptue L., von Overbeck J., Hampf H.

*Sequence of gp41env immunodominant region of HIV type 1 group O from

RT West Central Africa.^a;
RL AIDS Res. Hum. Retroviruses 13:901-904 (1997)
DR EMBL; U90132; AA66281.1; -
DR InterPro; IPR00328; Env-GR41.
DR Pfam; PF00517; GR41; 1.
KW Transmembrane.
MC

FT	NON_TER	SEQUENCE
1	1	105 AA; 12531 MW; 2D3D6B5BADC4A382 CRC64

Query Match	73.4%	Score 127;	DB 15;	Length 105
Best Local Similarity	71.4%;	Pred. No. 4e-12;		
Matches 20; Conservative	5;	Mismatches 3;		Indels

Qy	3	ETIMODQDRINSWGCKGRITCYTSARMH	30
		: : :	
Db	24	ETIMQNOQLINMGCKGKGLVCTYSVRMN	51

Search completed: June 20, 2002, 15:34:36
Job time: 214 sec

Fri Jun 21 10:39:08 2002

us-09-605-573a-69.rspt